

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: September 9, 2005, 10:16:59 / Search time 1710 Seconds  
(without alignments)  
1118.223 Million cell updates/sec

Title: US-09-981-151d-7  
Perfect score: 2895  
Sequence: 1 cgcctcgtatgtagcccg.....cccgggcttcctcccgcca 2895

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: Published Applications\_NA.\*  
2: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*  
3: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*  
19: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*  
20: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq.\*  
21: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq.\*  
22: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
23: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*  
24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2895	100.0	2895	US-09-981-151A-7	Sequence 7, Appli
2	2675.4	92.4	2997	US-09-981-151A-1	Sequence 1, Appli
3	1877.8	64.9	3675	US-10-330-176-1	Sequence 16, Appli
4	1877.8	64.9	3675	US-10-275-107-16	Sequence 3, Appli
5	1874.6	64.8	3675	US-10-217-774-3	Sequence 1, Appli
6	1874.6	64.8	3675	US-10-296-616-1	Sequence 3, Appli
7	1874.6	64.8	3675	US-10-804-457-3	Sequence 3, Appli

8	1874.6	64.8	4042	13	US-10-217-774-5	Sequence 5, Appli
9	1874.6	64.8	4042	21	US-10-804-457-5	Sequence 5, Appli
10	1795.6	62.0	2433	20	US-09-981-151A-3	Sequence 3, Appli
11	1695	58.5	2902	10	US-09-981-151A-5	Sequence 5, Appli
12	1638	56.6	4888	17	US-10-399-645-19	Sequence 19, Appli
13	709.6	24.5	3389	18	US-10-363-937-34	Sequence 34, Appli
14	708	24.5	3663	18	US-10-354-983-3	Sequence 3, Appli
15	708	24.5	3663	18	US-10-354-983-3	Sequence 1, Appli
16	708	24.5	3666	16	US-10-240-545A-1	Sequence 1, Appli
17	706.4	24.4	2805	18	US-10-275-107-18	Sequence 18, Appli
18	706.4	24.4	3246	19	US-10-391-364-88	Sequence 88, Appli
19	706.4	24.4	3445	19	US-10-391-364-88	Sequence 86, Appli
20	678.6	23.4	3630	17	US-10-161-493-123	Sequence 123, Appli
21	673.4	23.3	2589	14	US-10-226-560-1	Sequence 1, Appli
22	673.4	23.3	2589	22	US-10-990-935-1	Sequence 1, Appli
23	673.4	23.3	3013	14	US-10-188-186-131	Sequence 131, Appli
24	673.4	23.3	3013	14	US-10-228-560-3	Sequence 3, Appli
25	673.4	23.3	3013	22	US-10-990-935-3	Sequence 3, Appli
26	663	22.9	1476	13	US-10-217-774-1	Sequence 1, Appli
27	663	22.9	1476	21	US-10-804-457-1	Sequence 1, Appli
28	648.4	22.4	3555	17	US-10-188-186-129	Sequence 129, Appli
29	501	17.3	3954	18	US-10-354-983-5	Sequence 5, Appli
30	434.4	15.0	1059	17	US-10-161-493-129	Sequence 129, Appli
31	434.4	15.0	1059	17	US-10-161-493-133	Sequence 133, Appli
32	433.8	15.0	1586	18	US-10-354-983-7	Sequence 7, Appli
33	432.8	14.9	1059	17	US-10-161-493-125	Sequence 125, Appli
34	432.8	14.9	1059	17	US-10-161-493-127	Sequence 127, Appli
35	432.8	14.9	1059	17	US-10-161-493-131	Sequence 131, Appli
36	292.8	10.1	525	16	US-10-029-386-8689	Sequence 8689, Appli
37	292.8	10.1	348	16	US-10-029-386-22417	Sequence 22417, Appli
38	265.8	9.2	2052	14	US-10-103-377C-3	Sequence 3, Appli
39	265.8	9.2	2377	14	US-10-103-377C-1	Sequence 1, Appli
40	241.2	8.3	2217	14	US-10-226-560-6	Sequence 6, Appli
41	241.2	8.3	2217	22	US-10-990-935-6	Sequence 6, Appli
42	233.8	8.1	624	17	US-10-188-186-155	Sequence 155, Appli
43	227	7.8	2274	9	US-09-963-791-23	Sequence 23, Appli
44	227	7.8	2274	17	US-10-419-276-23	Sequence 23, Appli
45	227	7.8	2274	24	US-11-027-743-23	Sequence 23, Appli

#### ALIGNMENTS

RESULT 1  
US-09-981-151A-7  
; Sequence 7, Application US/09981151A  
; Publication No. US20030212256A1  
; GENERAL INFORMATION:  
; APPLICANT: Edinger, Shlomit R  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: MacDougall, John R  
; APPLICANT: Malyskar, Muriel M  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Peyman, John A  
; APPLICANT: Stone, David J  
; APPLICANT: Gunther, Erik  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Shimkets, Richard A  
; APPLICANT: Padigar, Muralidhara  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Patlurajan, Meera  
; APPLICANT: Taupier Jr, Raymond J  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Zernusen, Bryan D  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Szytek, Kimberly A  
; APPLICANT: Gangoli, Esha A  
; APPLICANT: Fernandes, Elma R  
; APPLICANT: Gorman, Linda  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-168  
; CURRENT APPLICATION NUMBER: US/09/981,151A

```

; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/241,040
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,058
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,063
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,243
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/242,152
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/242,482
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,611
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,612
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,880
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,881
; PRIOR FILING DATE: 2000-10-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2895
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-981-151A-7

Query Match      100.0%; Score 2895; DB 10; Length 2895;
Best Local Similarity 100.0%; Pred. No.0;
Matches 2895; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGCTCTGATGTAAGCCCGCGCGCGGATGCGGGGCTTGGCGGCGCTGTGATGCTG 60
DB      1 CGCTCTGATGTAAGCCCGCGCGCGGATGCGGGGCTTGGCGGCGCTGTGATGCTG 60

QY      61 TTGGCGAGGTGGCCGAGCAGTGAAGTCCCGGGCGCTCCCAACGCGGAAACCGCGG 120
DB      61 TTGGCGAGGTGGCCGAGCAGTGAAGTCCCGGGCGCTCCCAACGCGGAAACCGCGG 120

QY      121 TCCGGAAGCTGGAAGGCGAGTCCCGGGCGCTCTCCCGGGAGACCCCGCGCTGAC 180
DB      121 TCCGGAAGCTGGAAGGCGAGTCCCGGGCGCTCTCCCGGGAGACCCCGCGCTGAC 180

QY      121 TCCGGAAGCTGGAAGGCGAGTCCCGGGCGCTCTCCCGGGAGACCCCGCGCTGAC 180
DB      121 TCCGGAAGCTGGAAGGCGAGTCCCGGGCGCTCTCCCGGGAGACCCCGCGCTGAC 180

QY      181 GCGATGTCGCGCTGTTTTCCGAGGCACTGCTGCGCATGAGACCCGAGCGGACG 240
DB      181 GCGATGTCGCGCTGTTTTCCGAGGCACTGCTGCGCATGAGACCCGAGCGGACG 240

QY      241 GCGTGGAGCCGAGCGTCCCGGCTCTCTCCACCCGCGAGCGGCGCGGCTGATGA 300
DB      241 GCGTGGAGCCGAGCGTCCCGGCTCTCTCCACCCGCGAGCGGCGCGGCTGATGA 300

QY      241 GCGTGGAGCCGAGCGTCCCGGCTCTCTCCACCCGCGAGCGGCGCGGCTGATGA 300
DB      241 GCGTGGAGCCGAGCGTCCCGGCTCTCTCCACCCGCGAGCGGCGCGGCTGATGA 300

QY      301 AAAGGGCGGGAACA TGAATGAAGCTGAAACCAATGTTCTCAGAAACTAAACAAGAA 360
DB      301 AAAGGGCGGGAACA TGAATGAAGCTGAAACCAATGTTCTCAGAAACTAAACAAGAA 360

QY      301 AAAGGGCGGGAACA TGAATGAAGCTGAAACCAATGTTCTCAGAAACTAAACAAGAA 360
DB      301 AAAGGGCGGGAACA TGAATGAAGCTGAAACCAATGTTCTCAGAAACTAAACAAGAA 360

QY      361 GAAACCAAACTGATGTTCTCACTCAATATGACCTGCTCTGCTACGAGGTTGAC 420
DB      361 GAAACCAAACTGATGTTCTCACTCAATATGACCTGCTCTGCTACGAGGTTGAC 420

QY      361 GAAACCAAACTGATGTTCTCACTCAATATGACCTGCTCTGCTACGAGGTTGAC 420
DB      361 GAAACCAAACTGATGTTCTCACTCAATATGACCTGCTCTGCTACGAGGTTGAC 420

QY      421 CACAGGGGCGATTACGTGTCCTCAATAATGATGACCATCAGGCGGAGAAAGACATG 480
DB      421 CACAGGGGCGATTACGTGTCCTCAATAATGATGACCATCAGGCGGAGAAAGACATG 480

QY      421 CACAGGGGCGATTACGTGTCCTCAATAATGATGACCATCAGGCGGAGAAAGACATG 480
DB      421 CACAGGGGCGATTACGTGTCCTCAATAATGATGACCATCAGGCGGAGAAAGACATG 480

QY      481 GCGGTGTCGAGGTTGAGTCTCTTCACTTCCGCTGAAGGCGCGAGACACTTCCAC 540
DB      481 GCGGTGTCGAGGTTGAGTCTCTTCACTTCCGCTGAAGGCGCGAGACACTTCCAC 540

QY      481 GCGGTGTCGAGGTTGAGTCTCTTCACTTCCGCTGAAGGCGCGAGACACTTCCAC 540
DB      481 GCGGTGTCGAGGTTGAGTCTCTTCACTTCCGCTGAAGGCGCGAGACACTTCCAC 540

QY      541 ATGATCTGAGGCTTCCAGAGCCTAGTGGCTCTGGCTTTATTTGAGAGCTTGGAG 600
DB      541 ATGATCTGAGGCTTCCAGAGCCTAGTGGCTCTGGCTTTATTTGAGAGCTTGGAG 600
```

```

QY      601 AAGACAGCACTAAGTCTGTGCACTTTACCGGCAAGGACTTGTGTTATCAAGGC 660
DB      601 AAGACAGCACTAAGTCTGTGCACTTTACCGGCAAGGACTTGTGTTATCAAGGC 660

QY      661 TCTTTGGCATCAACAAGAACTGCGCATCGCATGAGGGAAGTTCTGAGGAGCTCCACT 720
DB      661 TCTTTGGCATCAACAAGAACTGCGCATCGCATGAGGGAAGTTCTGAGGAGCTCCACT 720

QY      661 TCTTTGGCATCAACAAGAACTGCGCATCGCATGAGGGAAGTTCTGAGGAGCTCCACT 720
DB      661 TCTTTGGCATCAACAAGAACTGCGCATCGCATGAGGGAAGTTCTGAGGAGCTCCACT 720

QY      721 CGCACTGTAAGCTTGAACAGTCAAGAAATGTCCTCCGAGAGTGTGACTTCCGTGCT 780
DB      721 CGCACTGTAAGCTTGAACAGTCAAGAAATGTCCTCCGAGAGTGTGACTTCCGTGCT 780

QY      721 CGCACTGTAAGCTTGAACAGTCAAGAAATGTCCTCCGAGAGTGTGACTTCCGTGCT 780
DB      721 CGCACTGTAAGCTTGAACAGTCAAGAAATGTCCTCCGAGAGTGTGACTTCCGTGCT 780

QY      781 GCTCAGTGTCCGAGCAACAAGCAGATTCAGAGGCGGCACTACAGTGAAGCCT 840
DB      781 GCTCAGTGTCCGAGCAACAAGCAGATTCAGAGGCGGCACTACAGTGAAGCCT 840

QY      781 GCTCAGTGTCCGAGCAACAAGCAGATTCAGAGGCGGCACTACAGTGAAGCCT 840
DB      781 GCTCAGTGTCCGAGCAACAAGCAGATTCAGAGGCGGCACTACAGTGAAGCCT 840

QY      841 TACACTCAAGTGAAGCCGACTTATGCAAACTCTGCTGTAATGCGAAGGATTTGATTC 900
DB      841 TACACTCAAGTGAAGCCGACTTATGCAAACTCTGCTGTAATGCGAAGGATTTGATTC 900

QY      841 TACACTCAAGTGAAGCCGACTTATGCAAACTCTGCTGTAATGCGAAGGATTTGATTC 900
DB      841 TACACTCAAGTGAAGCCGACTTATGCAAACTCTGCTGTAATGCGAAGGATTTGATTC 900

QY      901 TTTCTTTCTTTGTCAAAATGAAGTCAAGATGGAATCTCATGCTCGAGAGATGCGTAAT 960
DB      901 TTTCTTTCTTTGTCAAAATGAAGTCAAGATGGAATCTCATGCTCGAGAGATGCGTAAT 960

QY      901 TTTCTTTCTTTGTCAAAATGAAGTCAAGATGGAATCTCATGCTCGAGAGATGCGTAAT 960
DB      901 TTTCTTTCTTTGTCAAAATGAAGTCAAGATGGAATCTCATGCTCGAGAGATGCGTAAT 960

QY      961 GTTTGTATATGATGGATATGTAAGTCAAGTGTGTTGTCATCTGCGCAATGCCCGAG 1020
DB      961 GTTTGTATATGATGGATATGTAAGTCAAGTGTGTTGTCATCTGCGCAATGCCCGAG 1020

QY      961 GTTTGTATATGATGGATATGTAAGTCAAGTGTGTTGTCATCTGCGCAATGCCCGAG 1020
DB      961 GTTTGTATATGATGGATATGTAAGTCAAGTGTGTTGTCATCTGCGCAATGCCCGAG 1020

QY      1021 CCTCCCAAGGAAGACTCTTTCATCTGCGAGATGATTAAGTCTTGCTTACGGGATTAAG 1080
DB      1021 CCTCCCAAGGAAGACTCTTTCATCTGCGAGATGATTAAGTCTTGCTTACGGGATTAAG 1080

QY      1081 CGCTCTCTTGTGAGGTCCATAGAAATGAAGACTGAACGCTGAGACCTTGTGTGTC 1140
DB      1081 CGCTCTCTTGTGAGGTCCATAGAAATGAAGACTGAACGCTGAGACCTTGTGTGTC 1140

QY      1141 GACAAAAAGATGATGCAAAACCATGCGCATGAAATATCACCACTTACGTCTCAGATA 1200
DB      1141 GACAAAAAGATGATGCAAAACCATGCGCATGAAATATCACCACTTACGTCTCAGATA 1200

QY      1201 CTCAACATGATATCGCTTTATTCAAAAGATGATGAGGGAAGATGGGACTGTCAT 1260
DB      1201 CTCAACATGATATCGCTTTATTCAAAAGATGATGAGGGAAGATGGGACTGTCAT 1260

QY      1201 CTCAACATGATATCGCTTTATTCAAAAGATGATGAGGGAAGATGGGACTGTCAT 1260
DB      1201 CTCAACATGATATCGCTTTATTCAAAAGATGATGAGGGAAGATGGGACTGTCAT 1260

QY      1261 GACCAAGCATCTTACTGATCTGTGATATATGTTCTGGAAGAAAGAGCCCTGTGAC 1320
DB      1261 GACCAAGCATCTTACTGATCTGTGATATATGTTCTGGAAGAAAGAGCCCTGTGAC 1320

QY      1261 GACCAAGCATCTTACTGATCTGTGATATATGTTCTGGAAGAAAGAGCCCTGTGAC 1320
DB      1261 GACCAAGCATCTTACTGATCTGTGATATATGTTCTGGAAGAAAGAGCCCTGTGAC 1320

QY      1321 ACTTTGGGATTTGCAACCATTAAGTGAATGTGTAAATTCGACGCTGCAAGTTAAT 1380
DB      1321 ACTTTGGGATTTGCAACCATTAAGTGAATGTGTAAATTCGACGCTGCAAGTTAAT 1380

QY      1321 ACTTTGGGATTTGCAACCATTAAGTGAATGTGTAAATTCGACGCTGCAAGTTAAT 1380
DB      1321 ACTTTGGGATTTGCAACCATTAAGTGAATGTGTAAATTCGACGCTGCAAGTTAAT 1380

QY      1381 GAAAGTACAGGCTTTGCACTGGCCCTTCACTTGGCCCATGAGTCTGGAACAACCTTTGGC 1440
DB      1381 GAAAGTACAGGCTTTGCACTGGCCCTTCACTTGGCCCATGAGTCTGGAACAACCTTTGGC 1440

QY      1381 GAAAGTACAGGCTTTGCACTGGCCCTTCACTTGGCCCATGAGTCTGGAACAACCTTTGGC 1440
DB      1381 GAAAGTACAGGCTTTGCACTGGCCCTTCACTTGGCCCATGAGTCTGGAACAACCTTTGGC 1440

QY      1441 ATGATTCATGATGGAAGGAAGCAATGTGTAAAAAGTCCGAGGGAACATCATGTCCCT 1500
DB      1441 ATGATTCATGATGGAAGGAAGCAATGTGTAAAAAGTCCGAGGGAACATCATGTCCCT 1500

QY      1441 ATGATTCATGATGGAAGGAAGCAATGTGTAAAAAGTCCGAGGGAACATCATGTCCCT 1500
DB      1441 ATGATTCATGATGGAAGGAAGCAATGTGTAAAAAGTCCGAGGGAACATCATGTCCCT 1500

QY      1501 ACATTGGGAGGAGCAATGAGAGTCTTCTCTGTGTCACCTTGACGCGGCAATATTACAC 1560
DB      1501 ACATTGGGAGGAGCAATGAGAGTCTTCTCTGTGTCACCTTGACGCGGCAATATTACAC 1560

QY      1501 ACATTGGGAGGAGCAATGAGAGTCTTCTCTGTGTCACCTTGACGCGGCAATATTACAC 1560
DB      1501 ACATTGGGAGGAGCAATGAGAGTCTTCTCTGTGTCACCTTGACGCGGCAATATTACAC 1560

QY      1561 AAATTTCTAAGCACCGCTCAAGCTATCTGCGCTGCTGATCAGCCAAACCTGTGAAGAA 1620
DB      1561 AAATTTCTAAGCACCGCTCAAGCTATCTGCGCTGCTGATCAGCCAAACCTGTGAAGAA 1620

QY      1561 AAATTTCTAAGCACCGCTCAAGCTATCTGCGCTGCTGATCAGCCAAACCTGTGAAGAA 1620
DB      1561 AAATTTCTAAGCACCGCTCAAGCTATCTGCGCTGCTGATCAGCCAAACCTGTGAAGAA 1620

QY      1621 TACAAGTATCTGAGAAATTCGAGAGAAATTAATATGATGAAACACACAGTGCAGTGG 1680
DB      1621 TACAAGTATCTGAGAAATTCGAGAGAAATTAATATGATGAAACACACAGTGCAGTGG 1680
```

QY 1681 CAGTTCCGAGAGAAAGCCAAAGCTCTGCATGTGGACCTTTAAAAAGACATCTGTAAAGCC 1740  
DB 1681 CAGTTCCGAGAGAAAGCCAAAGCTCTGCATGTGGACCTTTAAAAAGACATCTGTAAAGCC 1740  
QY 1741 CTGTGTGTCATCTGTATTTGGAAGAAATGTGAGCTTAATTTATGCCAGCAGCAAGAGCC 1800  
DB 1741 CTGTGTGTCATCTGTATTTGGAAGAAATGTGAGCTTAATTTATGCCAGCAGCAAGAGCC 1800  
QY 1801 ACAATTTGTGGGCGATGACATGTGTGCGGGGAGAGACATGTGTGAAATATGTGATGAA 1860  
DB 1801 ACAATTTGTGGGCGATGACATGTGTGCGGGGAGAGACATGTGTGAAATATGTGATGAA 1860  
QY 1861 GGGCCCAAGCCCAACCCATGGCAGTGTGCGACTGTCTTTTGTGTCCCAATGTCTCCAGG 1920  
DB 1861 GGGCCCAAGCCCAACCCATGGCAGTGTGCGACTGTCTTTTGTGTCCCAATGTCTCCAGG 1920  
QY 1921 ACCTGCGGAGGGGAGATATCTCATAGAGTGTGCTCTGACACAAACCCCAAGCCATTCGAT 1980  
DB 1921 ACCTGCGGAGGGGAGATATCTCATAGAGTGTGCTCTGACACAAACCCCAAGCCATTCGAT 1980  
QY 1981 GGAAGGGAAGTTCTGTGAGGGGCTCCACTCGACCTGAAAGCTGTGCAACAGTCAAGAAATGT 2040  
DB 1981 GGAAGGGAAGTTCTGTGAGGGGCTCCACTCGACCTGAAAGCTGTGCAACAGTCAAGAAATGT 2040  
QY 2041 CCCCGGAGACAGTGTGACTTCCGTGTCTGCTGAGTGTGCGAGCAACAGCAGACGATTC 2100  
DB 2041 CCCCGGAGACAGTGTGACTTCCGTGTCTGCTGAGTGTGCGAGCAACAGCAGACGATTC 2100  
QY 2101 AGAGGGGGGCACTACAGTGGAGACCTTACACTAAGTAAAGATCGAGCTTATGCAAA 2160  
DB 2101 AGAGGGGGGCACTACAGTGGAGACCTTACACTAAGTAAAGATCGAGCTTATGCAAA 2160  
QY 2161 CTCTACTGTATGCGAGAAAGATTTGATTTCTCTCTTTCTTTGTCAATTAAGTCAAAAGAT 2220  
DB 2161 CTCTACTGTATGCGAGAAAGATTTGATTTCTCTCTTTCTTTGTCAATTAAGTCAAAAGAT 2220  
QY 2221 GGGAGCTTCATGCTCGAGAGATAGCCGTATGTTGTATAGTGGATATGTGAGAGAT 2280  
DB 2221 GGGAGCTTCATGCTCGAGAGATAGCCGTATGTTGTATAGTGGATATGTGAGAGAT 2280  
QY 2281 GGAATGTGACAAATGCTCTTGGATCTGAGTGTGAAAGCTCTGTGGGGGTGTGAACGGG 2340  
DB 2281 GGAATGTGACAAATGCTCTTGGATCTGAGTGTGAAAGCTCTGTGGGGGTGTGAACGGG 2340  
QY 2341 AATTAACCTCAGCTGCGACAGATTCACAGGGGTCTTACACCAAGACCAACCAACAG 2400  
DB 2341 AATTAACCTCAGCTGCGACAGATTCACAGGGGTCTTACACCAAGACCAACCAACAG 2400  
QY 2401 TATTTATCAGATGTGACATCTCTTCTGTGAGCCCGAGATATCCGATCTATGAATGAAC 2460  
DB 2401 TATTTATCAGATGTGACATCTCTTCTGTGAGCCCGAGATATCCGATCTATGAATGAAC 2460  
QY 2461 GTCTCTACCTCTCAATTTCTGTGCGCAATGCTCTCAAGAGTACTAAGTGGGAC 2520  
DB 2461 GTCTCTACCTCTCAATTTCTGTGCGCAATGCTCTCAAGAGTACTAAGTGGGAC 2520  
QY 2521 TGAGCCGTGAGCTGAGCCGCGCGGTCTCAAAATTTTGGGACCTACTTTTGACTACAGCGG 2580  
DB 2521 TGAGCCGTGAGCTGAGCCGCGCGGTCTCAAAATTTTGGGACCTACTTTTGACTACAGCGG 2580  
QY 2581 TCCCTATATAGAGCCCGAGAACTTAATGCTACTGAGCAACCAACGAGACATGATTTG 2640  
DB 2581 TCCCTATATAGAGCCCGAGAACTTAATGCTACTGAGCAACCAACGAGACATGATTTG 2640  
QY 2641 GAGCTGCTGTTTTCAGGGAGAAAGCCGGGGTGTGCTCTGAGAAATCTCAATGCTCTG 2700  
DB 2641 GAGCTGCTGTTTTCAGGGAGAAAGCCGGGGTGTGCTCTGAGAAATCTCAATGCTCTG 2700  
QY 2701 GGGAGCGAGAGAGAGCCCGCTGAGCCAGCAGTCACTTGGGCGATCGGCGCTGAG 2760  
DB 2701 GGGAGCGAGAGAGAGCCCGCTGAGCCAGCAGTCACTTGGGCGATCGGCGCTGAG 2760  
QY 2761 TGCTCCGTGTCTGTCGAGAGGGGGTATGAGTGTGCTTCAAGTGTGCTCTGAGAGCAGATGT 2820

DB 2761 TGCTCCGTGTCTGTCGAGAGGGGGTATGAGTGTGCTTCAAGTGTGCTCTGAGAGCAGCATGT 2820  
QY 2821 CAGCCTTCAGCCACTCGCTGATCATTTGCACTGGGCTTTCTTGAATCTTAATGAGCAGCCGG 2880  
DB 2821 CAGCCTTCAGCCACTCGCTGATCATTTGCACTGGGCTTTCTTGAATCTTAATGAGCAGCCGG 2880  
QY 2881 GGCTCTCCCTGCCA 2895  
DB 2881 GGCTCTCCCTGCCA 2895

RESULT 2  
US-09-981-151A-1  
Sequence 1, Application US/09981151A  
Publication No. US20030212256A1  
GENERAL INFORMATION:  
APPLICANT: Edinger, Shlomit R  
APPLICANT: Gerlach, Valerie  
APPLICANT: MacDougall, John R  
APPLICANT: Malvankar, Muriel M  
APPLICANT: Smithson, Glenda  
APPLICANT: Miller, Isabelle  
APPLICANT: Peyman, John A  
APPLICANT: Stone, David J  
APPLICANT: Gunther, Erik  
APPLICANT: Ellerman, Karen  
APPLICANT: Shinkets, Richard A  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Guo, Xiaojia  
APPLICANT: Patlurajan, Meera  
APPLICANT: Taupier Jr, Raymond J  
APPLICANT: Burgess, Catherine B  
APPLICANT: Zerhusen, Bryan D  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Spytek, Kimberly A  
APPLICANT: Gangoili, Saba A  
APPLICANT: Fernandes, Bima R  
APPLICANT: Gorman, Linda  
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-168  
CURRENT APPLICATION NUMBER: US/09/981,151A  
PRIOR FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 60/241,040  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,058  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,063  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,243  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/242,152  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/242,482  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,611  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,612  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,880  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/242,881  
PRIOR FILING DATE: 2000-10-24  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 2997  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (857)..(858)

OTHER INFORMATION: wherein n is an a or t or c or g.  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (2383)  
OTHER INFORMATION: wherein n is an a or t or c or g.  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (2983)  
OTHER INFORMATION: wherein n is an a or t or c or g.  
US-09-981-151A-1

Query Match 92.4%; Score 2675.4; DB 10; Length 2997;  
Best Local Similarity 94.9%; Pred. No. 0;

Matches 2866; Conservative 0; Mismatches 5; Indels 150; Gaps 4;

QY 1 CGCTCTGATGTAAGCCCGCGCGCGGATGAGCGGGCTTGGCGCGCTGTGATGCTG 60  
Db 1 CGCTCTGATGTAAGCCCGCGCGCGGATGAGCGGGCTTGGCGCGCTGTGATGCTG 60  
QY 61 TTGGCGAGGTGGCCGAGCAGGTGAGTCCGGGCGCTCCCAACGAGCGGAAACGGCGG 120  
Db 61 TTGGCGAGGTGGCCGAGCAGGTGAGTCCGGGCGCTCCCAACGAGCGGAAACGGCGG 120  
QY 121 TTGGCAGAGTGAAGGAGATCCCGCGGCTCTCTCCCGGAGACCCGCGCTCAC 180  
Db 121 TTGGCAGAGTGAAGGAGATCCCGCGGCTCTCTCCCGGAGACCCGCGCTCAC 180  
QY 181 GCGATGTCCGCGCTGTTTTCCGAGAGCACTGCGTGCAGCATGGACCCGACGCGCAG 240  
Db 181 GCGATGTCCGCGCTGTTTTCCGAGAGCACTGCGTGCAGCATGGACCCGACGCGCAG 240  
QY 241 GCGTGGAGACCCGAGGTCCTCTCTCCACCCGCGAGCGCGCGGCTGATGGA 300  
Db 241 GCGTGGAGACCCGAGGTCCTCTCTCCACCCGCGAGCGCGCGGCTGATGGA 300  
QY 301 AAAGGGGAGGACATGATGAAGTGAAGCAACATGTTCTGAGCAACTAACAAGAAACA 360  
Db 301 AAAGGGGAGGACATGATGAAGTGAAGCAACATGTTCTGAGCAACTAACAAGAAACA 360  
QY 361 GAAACCAAACTGATGTTCTCACTCAATATGACCTGGTCTCTGCTCAAGAGTTGAC 420  
Db 361 GAAACCAAACTGATGTTCTCACTCAATATGACCTGGTCTCTGCTCAAGAGTTGAC 420  
QY 421 CACAGGGGCGATTAAGTGTCCCAATGAATATGACCATGAGCGGCGAGAAAGACAGTG 480  
Db 421 CACAGGGGCGATTAAGTGTCCCAATGAATATGACCATGAGCGGCGAGAAAGACAGTG 480  
QY 481 GCGGTGCCGAGGTGAGTCTCTTCACTTCGCGCTGAAAGGCGCCAGGACGATCCAC 540  
Db 481 GCGGTGCCGAGGTGAGTCTCTTCACTTCGCGCTGAAAGGCGCCAGGACGATCCAC 540  
QY 541 ATGGATCTGAGGACTTCAGACAGCTAAGTGGCTCTGGCTTTATGTGACAGGTTGGAG 600  
Db 541 ATGGATCTGAGGACTTCAGACAGCTAAGTGGCTCTGGCTTTATGTGACAGGTTGGAG 600  
QY 601 AAGACAGGCACTAAGTGTGTGCACTTTAAGCGCAGAGAGACTTGTGTTTATCAAGGC 660  
Db 601 AAGACAGGCACTAAGTGTGTGCACTTTAAGCGCAGAGAGACTTGTGTTTATCAAGGC 660  
QY 661 TCTTTGAGATCAACAGAACTGCGCATGAGAGGAAAGTTCTGTGAGGGCTCACT 720  
Db 661 TCTTTGAGATCAACAGAACTGCGCATGAGAGGAAAGTTCTGTGAGGGCTCACT 720  
QY 721 CCGACTCTGAAGCTCTGCAACAGTCAAGAAATGTCCTCCGAGGACGTGTGACTTCG 780  
Db 721 CCGACTCTGAAGCTCTGCAACAGTCAAGAAATGTCCTCCGAGGACGTGTGACTTCG 780  
QY 781 GCTCAAGTGTCCGAGCAACAAGACAGATTTAGAGGGCGGCACTAACAAGTGAAGCCT 840  
Db 781 GCTCAAGTGTCCGAGCAACAAGACAGATTTAGAGGGCGGCACTAACAAGTGAAGCCT 840  
QY 841 TAACTCAAGTGAAGCGCACTATGCAAACTTAAGTATGACAGAAAGATTGATTC 900  
Db 841 TAACTCAAGTGAAGCGCACTATGCAAACTTAAGTATGACAGAAAGATTGATTC 900

Db 841 TAACTCAAGTGAAGGANNAGACTTATGCAAACTTAAGTATGACAGAAAGATTGATTC 900  
QY 901 TTCTTTCTTTGTCAATAAAGTCAAAAGATGAGGATCCATGCTCCGAGGATACCGTAA 960  
Db 901 TTCTTTCTTTGTCAATAAAGTCAAAAGATGAGGATCCATGCTCCGAGGATACCGTAA 960  
QY 961 GTTTGTATATGATGAGATATGAGTCAAGTGTGTGTCCATCTGCGCAGATGCCCGAG 1020  
Db 961 GTTTGTATATGATGAGATATGAGTCAAGTGTGTGTCCATCTGCGCAGATGCCCGAG 1020  
QY 1021 CCTCCCAAGGAGAGCTCTTCACTTGGCAGATGATTAAGCTTGTGTTAGGGCAATAG 1080  
Db 1021 CCTCCCAAGGAGAGCTCTTCACTTGGCAGATGATTAAGCTTGTGTTAGGGCAATAG 1080  
QY 1081 CGCTCTCTTGTGAGGTCCATGAAATGAAAGTGAAGCTGAGAGACCTTGTGTGTGTC 1140  
Db 1081 CGCTCTCTTGTGAGGTCCATGAAATGAAAGTGAAGCTGAGAGACCTTGTGTGTGTC 1140  
QY 1141 GACAAAAAGATGATGCAAAACATGCGCATGAAATATCAACCTAGTGTCTACAGATA 1200  
Db 1141 GACAAAAAGATGATGCAAAACATGCGCATGAAATATCAACCTAGTGTCTACAGATA 1200  
QY 1201 CTCAACATGATATCTGCTTTATCAAGA----- 1229  
Db 1201 CTCAACATGATATCTGCTTTATCAAGA----- 1229  
QY 1230 ----- 1229  
Db 1230 ----- 1229  
QY 1261 ATTGTAGTCTGATTTCTTAGAAGATGAAACAGCAGAGCTGTGATTAAGTCAACGCA 1320  
Db 1261 ATTGTAGTCTGATTTCTTAGAAGATGAAACAGCAGAGCTGTGATTAAGTCAACGCA 1320  
QY 1230 -----TGAATTGATGGGAAAGATGGGACT 1254  
Db 1230 -----TGAATTGATGGGAAAGATGGGACT 1254  
QY 1321 GACCAACCTTAAGTAGCTCTGCCAGTGGCAGTCTGATTAAGTGGGAAAGATGGGACT 1380  
Db 1321 GACCAACCTTAAGTAGCTCTGCCAGTGGCAGTCTGATTAAGTGGGAAAGATGGGACT 1380  
QY 1255 CGTCAATGACACGCGCATCTTACTGACTGATATATGTTCTCGGAAAGATGAGCCC 1314  
Db 1255 CGTCAATGACACGCGCATCTTACTGACTGATATATGTTCTCGGAAAGATGAGCCC 1314  
QY 1381 CGTCAATGACACGCGCATCTTACTGACTGATATATGTTCTCGGAAAGATGAGCCC 1440  
Db 1381 CGTCAATGACACGCGCATCTTACTGACTGATATATGTTCTCGGAAAGATGAGCCC 1440  
QY 1315 TGTGACACTTTGGGATTTGACCCCATTAAGTGAATGTGTAAATATCGAGCTGACG 1374  
Db 1315 TGTGACACTTTGGGATTTGACCCCATTAAGTGAATGTGTAAATATCGAGCTGACG 1374  
QY 1441 TGTGACACTTTGGGATTTGACCCCATTAAGTGAATGTGTAAATATCGAGCTGACG 1500  
Db 1441 TGTGACACTTTGGGATTTGACCCCATTAAGTGAATGTGTAAATATCGAGCTGACG 1500  
QY 1375 ATTAATGAAGATACAGTCTTGTGATGCGCTTACCATTTGCCATGAGCTTGGACACAC 1434  
Db 1375 ATTAATGAAGATACAGTCTTGTGATGCGCTTACCATTTGCCATGAGCTTGGACACAC 1434  
QY 1501 ATTAATGAAGATACAGTCTTGTGATGCGCTTACCATTTGCCATGAGCTTGGACACAC 1560  
Db 1501 ATTAATGAAGATACAGTCTTGTGATGCGCTTACCATTTGCCATGAGCTTGGACACAC 1560  
QY 1435 TTTGGCATGATTCATGATGAGAGAAAGAAATGTGTAAAGTCCGAGGCGCAATCATG 1494  
Db 1435 TTTGGCATGATTCATGATGAGAGAAAGAAATGTGTAAAGTCCGAGGCGCAATCATG 1494  
QY 1561 TTTGGCATGATTCATGATGAGAGAAAGAAATGTGTAAAGTCCGAGGCGCAATCATG 1620  
Db 1561 TTTGGCATGATTCATGATGAGAGAAAGAAATGTGTAAAGTCCGAGGCGCAATCATG 1620  
QY 1495 TCCCTTAATTTGGCAGACGCAATGAGTCTTCTCTGTGCACTCTGACCGCGCAGTAT 1554  
Db 1495 TCCCTTAATTTGGCAGACGCAATGAGTCTTCTCTGTGCACTCTGACCGCGCAGTAT 1554  
QY 1621 TCCCTTAATTTGGCAGACGCAATGAGTCTTCTCTGTGCACTCTGACCGCGCAGTAT 1680  
Db 1621 TCCCTTAATTTGGCAGACGCAATGAGTCTTCTCTGTGCACTCTGACCGCGCAGTAT 1680  
QY 1555 CTACACAAATTTCTAAGACCGCTTAAGCTATCTGCTTGTGATCAACCAAAAGCTGTG 1614  
Db 1555 CTACACAAATTTCTAAGACCGCTTAAGCTATCTGCTTGTGATCAACCAAAAGCTGTG 1614  
QY 1681 CTACACAAATTTCTAAGACCGCTTAAGCTATCTGCTTGTGATCAACCAAAAGCTGTG 1740  
Db 1681 CTACACAAATTTCTAAGACCGCTTAAGCTATCTGCTTGTGATCAACCAAAAGCTGTG 1740  
QY 1615 AAGAAATCAAGTATCTGAGAAATTTGCCAGAGAAATTAATATGATGCAAAACACAGTGC 1674  
Db 1615 AAGAAATCAAGTATCTGAGAAATTTGCCAGAGAAATTAATATGATGCAAAACACAGTGC 1674  
QY 1741 AAGAAATCAAGTATCTGAGAAATTTGCCAGAGAAATTAATATGATGCAAAACACAGTGC 1800  
Db 1741 AAGAAATCAAGTATCTGAGAAATTTGCCAGAGAAATTAATATGATGCAAAACACAGTGC 1800  
QY 1675 AAGTGGCAGTTCGAGAGAAAGCAAGCTCTGATGCTGACCTTTAAAAAGGACATCTGT 1734  
Db 1675 AAGTGGCAGTTCGAGAGAAAGCAAGCTCTGATGCTGACCTTTAAAAAGGACATCTGT 1734  
QY 1801 AAGTGGCAGTTCGAGAGAAAGCAAGCTCTGATGCTGACCTTTAAAAAGGACATCTGT 1860  
Db 1801 AAGTGGCAGTTCGAGAGAAAGCAAGCTCTGATGCTGACCTTTAAAAAGGACATCTGT 1860  
QY 1735 AAAAGCTGTGTGTGCAATCTGATTTGGAAGAAATGTGAGCTTAATTTATGCGACACAGA 1794  
Db 1735 AAAAGCTGTGTGTGCAATCTGATTTGGAAGAAATGTGAGCTTAATTTATGCGACACAGA 1794  
QY 1861 AAAAGCTGTGTGTGCAATCTGATTTGGAAGAAATGTGAGCTTAATTTATGCGACACAGA 1920  
Db 1861 AAAAGCTGTGTGTGCAATCTGATTTGGAAGAAATGTGAGCTTAATTTATGCGACACAGA 1920  
QY 1795 GAAAGCAAAATTTGGGACATGACATGTGTGCGGAGAGACAGTGTGTGAAATATGAT 1854  
Db 1795 GAAAGCAAAATTTGGGACATGACATGTGTGCGGAGAGACAGTGTGTGAAATATGAT 1854  
QY 1921 GAAAGCAAAATTTGGGACATGACATGTGTGCGGAGAGACAGTGTGTGAAATATGAT 1980  
Db 1921 GAAAGCAAAATTTGGGACATGACATGTGTGCGGAGAGACAGTGTGTGAAATATGAT 1980



QY	1855	GATGAAGGCCCAAGCCCAACCAATGAGCACTGCTGCGACTGCTCTTGGCTCCCAATGC	1914
Db	1981	GATGAAGGCCCAAGCCCAACCAATGAGCACTGCTGCGACTGCTCTTGGCTCCCAATGC	2040
QY	1915	TCGAGGACTGTCGAGAGGGGAGTATCTCATAGAGTCGCTCTGCACCCAACTCCAAAGCCA	1974
Db	2041	TCCAGGACTGTCGAGAGGGGAGTATCTCATAGAGTCGCTCTGCACCCAACTCCAAATCCA	2100
QY	1975	TCGATGAGAGGGAAGTTCTGTGAGGGGCTCCACTGCACTCTGAAAGCTCTGGAACAGTCAG	2034
Db	2101	TCGATGAGAGGGAAGTTCTGTGAGGGGCTCCACTGCACTCTGAAAGCTCTGGAACAGTCAG	2160
QY	2035	AAATGTCCCGGGGACAGGTGTGACTTCCGTCCTGCTCAGTGTGCGAGCACAAGCAGA	2094
Db	2161	AAATGTCCCGGGGACAGGTGTGACTTCCGTCCTGCTCAGTGTGCGAGCACAAGCAGA	2220
QY	2095	CGATTCAAGAGGGCGGCACTACAGTGGAGCCTTACACTCAAGTAAAGATCAGAGACTTA	2154
Db	2221	CGATTCAAGAGGGCGGCACTACAGTGGAGCCTTACACTCAAGTAAAGATCAGAGACTTA	2262
QY	2155	TGCAAACTCTATCTGATATGCGAAGAGATTAATTTCTTTTCTTTGTCAATAAAGTCC	2214
Db	2283	TGCAAACTCTATCTGATATGCGAAGAGATTAATTTCTTTTCTTTGTCAATAAAGTCC	2322
QY	2215	AAAGATGGGACTCCATGCTCGAGAGATAGCCGTATGTTTGTATATGATGGAGATATGTAG	2274
Db	2323	AAAGATGGGACTCCATGCTCGAGAGATAGCCGTATGTTTGTATATGATGGAGATATGTAG	2382
QY	2275	AGAGTTGGATGTGACATATGTCTTGGATCTGATCTGTGTAAAGACGTCTGTGGGTGTCT	2334
Db	2383	---ATTGATGTGTGCAATGTCCTTGGAACTGATCTGTGTAAAGACGTCTGTGGGTGTCT	2439
QY	2335	AACGGGAATAACTCAGCGCTGCAGCAATTCACAGGGGTCTCTACACAAGACACACACACC	2394
Db	2440	AACGGGAATAACTCAGCGCTGCAGCAATTCACAGGGGTCTCTACACAAGACACACACACC	2499
QY	2395	AACCAATTAATCACATGTGTACCAATTCCTTCTGGAGCCGAGATCCGATCTATGAA	2454
Db	2500	AAAC---ATTATATCATGTGTACCAATTCCTTCTGGAGCCGAGATTCGATCTATGAA	2556
QY	2455	ATGAACGCTCTACCTCTCTCAATTTCTGTGGCAATGCCCCAAGAGTATACCTGAAT	2514
Db	2557	ATGAACGCTCTACCTCTCTCAATTTCTGTGGCAATGCCCCAAGAGTATACCTGAAT	2616
QY	2515	GGGCACTGGAACCGTGAACCTGGCCCCGGCCGGATACAAATTTTGGGCACTACTTTGCACTAC	2574
Db	2617	GGGCACTGGAACCGTGAACCTGGCCCCGGCCGGATACAAATTTTGGGCACTACTTTGCACTAC	2676
QY	2575	AGAGGTCCTTAATATGAGCCCGGAGAACTTAATGCTACTGGAACCAACCAAGAACACTG	2634
Db	2677	AGAGGTCCTTAATATGAGCCCGGAGAACTTAATGCTACTGGAACCAACCAAGAACACTG	2736
QY	2635	ATTGTGAGCTGCTGTTTCAGGGAAGAACCCGGGTGTGTCTGGAAATACTCATGCTCT	2694
Db	2737	ATTGTGAGCTGCTGTTTCAGGGAAGAACCCGGGTGTGTCTGGAAATACTCATGCTCT	2796
QY	2695	CGCTTTGGGGAACCGAAGACAGCCCCCTGACCAGCCCAAGCTACACTTGGGCTATGTGCGC	2754
Db	2797	CGCTTTGGGGAACCGAAGACAGCCCCCTGACCAGCCCAAGCTACACTTGGGCTATGTGCGC	2856
QY	2755	TCATAGAGTCGCGGTCTCTGCGAGAGGGGGTATAGTGCTTCCAGAGCTGCTCTGGAAGCA	2814
Db	2857	TCATAGAGTCGCGGTCTCTGCGAGAGGGGGTATAGTGCTTCCAGAGCTGCTCTGGAAGCA	2916
QY	2815	GCATGTCAAGCTTCAAGCCACTGCGTACATTGCACTGGCTTTCTTGAATCTTAATGACA	2874
Db	2917	GCATGTCAAGCTTCAAGCCACTGCGTACATTGCACTGGCTTTCTTGAATCTTAATGACA	2976
QY	2875	GCCCGGGGCTTCTCCCTGCCA	2895
Db	2977	GCCCGAGGCTTCTCCCTGCCA	2997

Query	Match	64.9%	Score 1877.8	DB 17	Length 3675
US-10-330-176-1	Sequence 1, Application US/10330176				
	Publication No. US20030228676A1				
	GENERAL INFORMATION:				
	APPLICANT: Agostino, Michael				
	APPLICANT: DiIasio, Elizabeth				
	TITLE OF INVENTION: AGGRECANASE MOLECULES				
	FILE REFERENCE: AMI00884				
	CURRENT APPLICATION NUMBER: US/10/330.176				
	CURRENT FILING DATE: 2002-12-30				
	PRIOR APPLICATION NUMBER: 60/344,895				
	PRIOR FILING DATE: 2001-12-31				
	NUMBER OF SEQ ID NOS: 18				
	SOFTWARE: Patentin version 3.1				
	SEQ ID NO 1				
	LENGTH: 3675				
	TYPE: DNA				
	ORGANISM: Homo sapiens				
	US-10-330-176-1				
Query	Match	64.9%	Score 1877.8	DB 17	Length 3675
	Best Local Similarity	84.4%	Pred. No. 0		
	Matches 2289	Conservative 0	Mismatches 177	Indels 245	Gaps 6
Qy	202 GCAGGACCTGCGCTGCGCCCATGGGACCCCGCAGCGCGACGGCTTGAGAGCCCGAGCGTCC				261
Db	69 GCAGGACCTGCGCTGCGCCCATGGGACCCCGCAGCGCGACGGCTTGAGAGCCCGAGCGTCC				128
Qy	262 GCGTCTCTCTCCACCCCGGAGCGCGCGCTGATGGAAAAAGGCGGACATGATGAA				321
Db	129 GCGTCTCTCTCCACCCCGGAGCGCGCGCTGATGGAAAAAGGCG-----				175
Qy	322 GCTGAAACCATGCTTCTCAGCAAACTPAACAAGAAACAAACACTGCACTT				381
Db	176 -----				175
Qy	382 CTCACCTAATATGACGTGCTCTGCTTACGAGGTTGACCAAGGCGCATTAAGTCTC				441
Db	176 -----AATATGACGTGCTCTGCTTACGAGGTTGACCAAGGCGCATTAAGTCTC				228
Qy	442 CATTAAATCATGACCATCATGACGCGGAGAGACAGTGGCCGTCCGAGGTTGAGTCT				501
Db	229 CATGAATCATGACCATCATGACGCGGAGAGACAGTGGCCGTCCGAGGTTGAGTCT				288
Qy	502 CTTCACTTGGGCTGAAAGGCCCGACGACGACTTTCACATGATCTGAGACTTCCAGC				561
Db	289 CTTCACTTGGGCTGAAAGGCCCGACGACGACTTTCACATGATCTGAGACTTCCAGC				348
Qy	562 AGCCTATGGCTCCTGGCTTATATGTCAGACGTTGGGAAAGACAGGACCTAAGTCTGTG				621
Db	349 AGCCTATGGCTCCTGGCTTATATGTCAGACGTTGGGAAAGACAGGACCTAAGTCTGTG				408
Qy	622 CAGACTTTACCGCCAGAGAGACTTCTGTTTCTATCAAGGCTCTTGGCATCAACAGAAAC				681
Db	409 CAGACTTTACCGCCAGAGAGACTTCTGTTTCTATCAAGGCTCTTGGCATCAACAGAAAC				468
Qy	682 TCGCCATCGATGAGGAGAAATTCTGTGAGGGCTCCACTCGCACTTGAACTCTGCAAC				741
Db	469 TCCTCA-----GTGGCCCTTTCAACTCGCAAGGCTGTGCA				504
Qy	742 AGTCAGAAATGTCCCGCGGACAGTGTGACTTCCGCTGTCTAGTGTCCGACCAACAC				801
Db	505 GGCATGATACGAACAGAAAGGACGATTACTCTTAAAGGCCACTTCCACACTCTCA				564
Qy	802 AGCAGACGATTTAGAGGGCGGACCTAACAGTGG--AAGCTTACACTCAAGTAAAGCCG				859
Db	565 TGGAAATTCGGCAGAGCTGCCCAAGGACGCTGCGCATCCACGTAAGTAAAGAAATCC				624
Qy	860 ACTTATGCAAACTCTACTGTATGCGAAGAGATTGATTTCTTTCTTTTGTCAATA				919
Db	625 ACAGAGCCCATGCTCTCGGGGCGCAGTAGAGTCTCGTGAACCTC-----AAGG				672

QY 920 AAGTCAAGATGGAGCTCCATGCTCGGAGGATAGCCGTAAATGTTTGTATAGATGGATAT 979  
DB 673 ACATGGAGCTGGGACATCAACCCCTGCACAGCAGCACTTCGCTGGAGACTGGCCACAA 732  
QY 980 GTAGAGCTCATGTGTGTCCACATCTGC -GCACATGGCCCAAGCTCCCAAGAAAGCTTC 1038  
DB 733 AAGACGATTTCTGTGGAGAGCGCAAAATATACATGCCCCAGCTCCCAAGAAAGCTTC 792  
QY 1039 TTGATCTTGGCAGATGAGTATTAAGTCTTGCTTAACGATTAAGCGCTCTCTTGAAGTCC 1098  
DB 793 TTGATCTTGGCAGATGAGTATTAAGTCTTGCTTAACGATTAAGCGCTCTCTTGAAGTCC 852  
QY 1099 CATGAAATGAAAGAACTGAACTGTGAGAGACCTTGTGTGTGTGCACAAAAGATGATGCA 1158  
DB 853 CATGAAATGAAAGAACTGAACTGTGAGAGACCTTGTGTGTGTGCACAAAAGATGATGCA 912  
QY 1159 AACCATGGCCATGAAATATCACCACTAGTGTCTACGATCTCAACATGATGATCTGCT 1218  
DB 913 AACCATGGCCATGAAATATCACCACTAGTGTCTACGATCTCAACATGATGATCTGCT 972  
QY 1219 TTATTCAAAGA----- 1229  
DB 973 TTATTCAAAGATGGAACAATAGAGAAACATCAACTTGCAATGTAGGTCTGATTTCTT 1032  
QY 1230 ----- 1229  
DB 1033 CTAGAAATGAAAGAGCCAGAGCTGTGTATAGTACCAACGACAGACCACTTAAAGTAC 1092  
QY 1230 -----TGAATTGATGGGGAAGATGGGAGCTGTGTATGACAGCGCATC 1272  
DB 1093 TTCTGCCAGTGGCAGCTGTGATTTGATGGGAAAGATGGGAGCTGTGTATGACAGCGCATC 1152  
QY 1273 TTACTGATGTGTGTATATATGTTCTGTGAAAGATGAGCCCTGTGATCACTTTGGATTT 1332  
DB 1153 TTACTGATGTGTGTATATATGTTCTGTGAAAGATGAGCCCTGTGATCACTTTGGATTT 1212  
QY 1333 GCACCCATTAAGTGAATGTGTATTAATTCGACGCTGACGATTAATGAAGATACAGGT 1392  
DB 1213 GCACCCATTAAGTGAATGTGTATTAATTCGACGCTGACGATTAATGAAGATACAGGT 1272  
QY 1393 CTGGAAGTGGCTTCAACCATTTGCCATGAGTCTGGAACAACCTTGGCATGATTCATGAT 1452  
DB 1273 CTGGAAGTGGCTTCAACCATTTGCCATGAGTCTGGAACAACCTTGGCATGATTCATGAT 1332  
QY 1453 GGAAGAGGAAACATGTGTAAAAAGTCCGAGGGAACATCATGTCTCCCTACATTTGGCAGGA 1512  
DB 1333 GGAAGAGGAAACATGTGTAAAAAGTCCGAGGGAACATCATGTCTCCCTACATTTGGCAGGA 1392  
QY 1513 CGCAATGGAGTCTTCTCTGTGTCAACCTGTGACGCCGCAATCTACACAAATTTCTAAGC 1572  
DB 1393 CGCAATGGAGTCTTCTCTGTGTCAACCTGTGACGCCGCAATCTACACAAATTTCTAAGC 1452  
QY 1573 ACCGCTCAAGCTATCTGCTTGTGCTGATCAGCCAAAGCTGTGAAGAAATTCAGATTCCT 1632  
DB 1453 ACCGCTCAAGCTATCTGCTTGTGCTGATCAGCCAAAGCTGTGAAGAAATTCAGATTCCT 1512  
QY 1633 GAGAAATTCGACAGAGAAATTAATGATGCAACAACAGTGAAGTGTGAGTTCGAGAG 1692  
DB 1513 GAGAAATTCGACAGAGAAATTAATGATGCAACAACAGTGAAGTGTGAGTTCGAGAG 1572  
QY 1693 AAAGCCCAAGTCTGTGATGCTGTGAACTTTAAAAAGACATCTGTAAAGCCCTGTGTGCTCAT 1752  
DB 1573 AAAGCCCAAGTCTGTGATGCTGTGAACTTTAAAAAGACATCTGTAAAGCCCTGTGTGCTCAT 1632  
QY 1753 CGTATTGGAAGAAATGTGAGCTAAATTTATGCGACGACAGAGAGCAATTTGTGGG 1812  
DB 1633 CGTATTGGAAGAAATGTGAGCTAAATTTATGCGACGACAGAGAGCAATTTGTGGG 1692  
QY 1813 CATGACATGTGTGTGCGGGGAGACAGTGTGTGAAATATGTGTATGAAGGCCCAAGGCC 1872  
DB 1693 CATGACATGTGTGTGCGGGGAGACAGTGTGTGAAATATGTGTATGAAGGCCCAAGGCC 1752

QY 1873 ACCCATGGCCACTGTGTGAGCTGTCTTCTGTGTCCCAATGCTTCCAGACCTTGGAGGG 1932  
DB 1753 ACCCATGGCCACTGTGTGAGCTGTCTTCTGTGTCCCAATGCTTCCAGACCTTGGAGGG 1812  
QY 1933 GAGATATCTCATAGAGTGTGCTGTGACCAACCCCAAGCCATTCGATGAGAGAACTTC 1992  
DB 1813 GAGATATCTCATAGAGTGTGCTGTGACCAACCCCAAGCCATTCGATGAGAGAACTTC 1872  
QY 1993 TGTGAGGGCTCCACTGCGACCTGTGAAGCTTGTCAACAGTCAGAAATGTGTCCCGGACAT 2052  
DB 1873 TGTGAGGGCTCCACTGCGACCTGTGAAGCTTGTCAACAGTCAGAAATGTGTCCCGGACAT 1932  
QY 2053 GTTGAATTCGTGTGTGTGATGTGTGCGGACCAACAGACAGATTCAGAGGGCGGAC 2112  
DB 1933 GTTGAATTCGTGTGTGTGATGTGTGCGGACCAACAGACAGATTCAGAGGGCGGAC 1992  
QY 2113 TACAAGTGAAGCCCTTACCTCAAGTGAAGATTCAGAGCTTATGCAAACTCATCTATAC 2172  
DB 1993 TACAAGTGAAGCCCTTACCTCAAGTGAAGATTCAGAGCTTATGCAAACTCATCTATAC 2052  
QY 2173 GCAGAAAGATTTGATTTCTTTCTTTCTTTGTCAAATTAAGTCAAAAGATGGACTCCATGC 2232  
DB 2053 GCAGAAAGATTTGATTTCTTTCTTTCTTTGTCAAATTAAGTCAAAAGATGGACTCCATGC 2112  
QY 2233 TCGAGAGATAGCCGTATATGTTTGTATAGTGGATATGTGAGAGATTTGATGTGACAT 2292  
DB 2113 TCGAGAGATAGCCGTATATGTTTGTATAGTGGATATGTGAGAGATTTGATGTGACAT 2172  
QY 2293 GTCTTGTGATGTGATGTGTGAAGACGTGTGTGGGGTGTGTAAACGGAATTAACCTAGCC 2352  
DB 2173 GTCTTGTGATGTGATGTGTGAAGACGTGTGTGGGGTGTGTAAACGGAATTAACCTAGCC 2232  
QY 2353 TGCACGATTCACAGGGGTCTCTACACCAAGCACCAACACCAACAGATTTATTCACATG 2412  
DB 2233 TGCACGATTCACAGGGGTCTCTACACCAAGCACCAACACCAACAGATTTATTCACATG 2292  
QY 2413 GTACCAATTCCTTCTGTGAGCCCGGAGTATCCGATCTATGAATGAAGTCTTACCTCC 2472  
DB 2293 GTACCAATTCCTTCTGTGAGCCCGGAGTATCCGATCTATGAATGAAGTCTTACCTCC 2352  
QY 2473 TACATTTCTGTGCGAAATGCTCTCAGAAAGTATCTACGAAATGGGACCTGACCGTGCAC 2532  
DB 2353 TACATTTCTGTGCGAAATGCTCTCAGAAAGTATCTACGAAATGGGACCTGACCGTGCAC 2412  
QY 2533 TGGCCCGGCGGTACAAATTTTCGGGCACTACTTTGACATACAGACGCTCTATATGAG 2592  
DB 2413 TGGCCCGGCGGTACAAATTTTCGGGCACTACTTTGACATACAGACGCTCTATATGAG 2472  
QY 2593 CCCGGAATTAATGTGTATCTGTGACCAACCAACGAGACATGTGTGAGTGTCTGTTT 2652  
DB 2473 CCCGGAATTAATGTGTATCTGTGACCAACCAACGAGACATGTGTGAGTGTCTGTTT 2532  
QY 2653 CAGGGAAGAAACCCGGGTGTGTGCTGGGAATACTCATGCTGTGTGGGACGAGAG 2712  
DB 2533 CAGGGAAGAAACCCGGGTGTGTGCTGGGAATACTCATGCTGTGTGGGACGAGAG 2592  
QY 2713 CAGCCCTGTGCCAGCCAGCTACACTTGTGGGCAATGTGCGCTGTGAGTCTCGGTGTC 2772  
DB 2593 CAGCCCTGTGCCAGCCAGCTACACTTGTGGGCAATGTGCGCTGTGAGTCTCGGTGTC 2652  
QY 2773 TGGCGAGGGGG 2783  
DB 2653 TGGCGAGGGGG 2663

RESULT 4  
US-10-275-107-15  
; Sequence 16, Application US/10275107  
; Publication No. US20040063107A1  
; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, GREGORY D.  
; APPLICANT: WHYRE, DAVID  
; APPLICANT: SUDARSHANAM, SUCHA

```

? APPLICANT: MANNING, GERARD
? APPLICANT: CAENEPEL, SEAN R.
? APPLICANT: PAYNE, VILIA
? TITLE OF INVENTION: NOVEL PROTEASES
? FILE REFERENCE: 038602/1479
? CURRENT APPLICATION NUMBER: US/10/275.107
? CURRENT FILING DATE: 2003-11-03
? PRIOR APPLICATION NUMBER: PCT/US01/14431
? PRIOR FILING DATE: 2001-05-04
? PRIOR APPLICATION NUMBER: 60/201,879
? PRIOR FILING DATE: 2000-05-04
? NUMBER OF SEQ ID NOS: 105
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 16
? LENGTH: 3675
? TYPE: DNA
? ORGANISM: Homo sapiens
? OS-10-275-107-16

```

Query Match	64.9%	Score 1877.8;	DB 18;	Length 3675;
Best Local Similarity	84.4%	Pred. No. 0;		
Matches 2289; Conservative	0;	Mismatches 177;	Indels 245;	Gaps 6;

Qy	202	GCAGGACCTGCGGCGCATATGGAGACCCGACACGCGACTGGAGACCCGAGGTCCTC	261
Db	69	GCAGGACCTGCGGCGCATATGGAGACCCGACACGCGACTGGAGACCCGAGGTCCTC	128
Qy	262	GCGTCTCTTCCACCGCGAGCGCGCGGCTGTGATGGAAAAAGGCGCGGACATGGATGA	321
Db	129	GCGTCTCTTCCACCGCGAGCGCGCGGCTGTGATGGAAAAAGGCGCGG	175
Qy	322	GCTGGAAACCATCGTCTCAGCAAACTAACACAGAACAGAAAAACAAACCTGCATGTT	381
Db	176	-----	175
Qy	382	CTCACTCAATATGACTGTGCTCTGCGCTACAGAGTTGACACAGGCGCGATTACGTGCTC	441
Db	176	-----AAATGACCTGTGCTCTGCGCTACAGAGTTGACACAGGCGCGATTACGTGCTC	228
Qy	442	CATGAATATCATGACCATCAACGCGCGAGAAAGACATGGCGCGTGTCCGAGTTGAGTCT	501
Db	229	CATGAATATCATGACCATCAACGCGCGAGAAAGACATGGCGCGTGTCCGAGTTGAGTCT	288
Qy	502	CTTCACTTGGCGCTGGAAAGGCGCGACAGACATTTCCAATGATCTGAGAGACTTCCAGC	561
Db	289	CTTCACTTGGCGCTGGAAAGGCGCGACAGACATTTCCAATGATCTGAGAGACTTCCAGC	348
Qy	562	AGCCTAGTGCTCTCGCTTATTTGTGCAGACGTTGGAAAGACAGGCACTAAGCTGTG	621
Db	349	AGCCTAGTGCTCTCGCTTATTTGTGCAGACGTTGGAAAGACAGGCACTAAGCTGTG	408
Qy	622	CAGACTTTAACCGCAGAGAGACTTGTGTTCTATCAAGGCTCTTTGCGATCAACAGAAAC	681
Db	409	CAGACTTTAACCGCAGAGAGACTTGTGTTCTATCAAGGCTCTTTGCGATCAACAGAAAC	468
Qy	682	TTCGCATTCGCATGGAGGGAAGTTCTGTGAGGGCTTCACCTGCACTGTGAAGCTCTGCAAC	741
Db	469	TTCCTCA-----GTGGCCCTTTAACTCTGCAAGGCTTGTC	504
Qy	742	AGTCAGAAATGTCCCGGAGCAGTGTGACTTCGCTGCTCAGTGTCCGAGACACAAAC	801
Db	505	GGCATGTATCGAAGACAGAAAGAGCAGATTACTTCTTAAGGCGCACTTCTTCAACCTCTCA	564
Qy	802	AGCAGAGATTTCAAGAGGCGCGCACTTACAAAGTG--AAGCTTAACTCAAGTAAAGCGG	859
Db	565	TGGAAATTCGAGCAGCTGCCCAAGGCAAGCTGCGCATCCACGTAAGTAAAGAGATCC	624
Qy	860	ACTATATCAAACTACTATGTATCGCAGAGAGATTTGATTTCTTCTTTTCTTGTCAATA	919
Db	625	ACAGAGCCCATGCTCTTGGGCGCAGTAGAGTCTCTGTGACCTC-----AAGG	672
Qy	920	AAGTCAAAAGATGGAGCTTCATGCTTCGAGAGATAGCCGTAATGTTTGTATAGATGGATAT	979

Db	673	ACATGGAGCTGGGACATCAACCCCTGCA	CAGCGACCTTGCGCTGGGACTGCCACA	732	
Qy	980	GTGAGCTCAGTGTGSGTCCACATCTGC	-GCACATGCCAGCCTCCAGAGAACCTC	1038	
Db	733	AAGCAGCATTTCTGTGGAAGCCGAGAA	AAATPACATGCCCCAGCCTCCAGAGAACCTC	792	
Qy	1039	TTCACTCTTCCAGATGAGTATTAAGTCT	TTTGCTTACGGCATAAAGCGCTCTTTCTGAGTCC	1098	
Db	793	TTCACTCTTCCAGATGAGTATTAAGTCT	TTTGCTTACGGCATAAAGCGCTCTTTCTGAGTCC	852	
Qy	1099	CATGAATGAATGAAGACGGAACGTGG	AACCTGGTGGTCGACAAAAGATGATGCA	1158	
Db	853	CATGAATGAATGAAGACGGAACGTGG	AACCTGGTGGTCGACAAAAGATGATGCA	912	
Qy	1159	AACCATGGCCATGAAAAATATCACCA	CCCTAGCGTCCAGATACCAACATGATCTCT	1218	
Db	913	AACCATGGCCATGAAAAATATCACCA	CCCTAGCGTCCAGATACCAACATGATCTCT	972	
Qy	1219	TTATTCAAAG-----	-----	1229	
Db	973	TTATTCAAAGTGGAAACAAATAGAG	AAACATCAATTCGAAATTTGAGTCTGATCTT	1032	
Qy	1230	-----	-----	1229	
Db	1033	CTAGAAAGATGAACACCGACGATG	ATAGTCAACGACGACACCTTAATGATG	1092	
Qy	1230	-----	-----	1229	
Db	1093	TTCTGCAAGTGGCGAGTGTGATTTGA	TGGGGAAGATGGGACTGTATGACACG	1152	
Qy	1273	TTACTGACTGAGTCTGATATATGTTCT	CTGGAAGATGAGCCCTGTGACACTTTGGATTT	1332	
Db	1153	TTACTGACTGAGTCTGATATATGTTCT	CTGGAAGATGAGCCCTGTGACACTTTGGATTT	1212	
Qy	1333	GCACCCATATGTGGAATGTGTAAATAT	TCGACGTGCACGATTAATGAAGATACAGT	1392	
Db	1213	GCACCCATATGTGGAATGTGTAAATAT	TCGACGTGCACGATTAATGAAGATACAGT	1272	
Qy	1393	CTTGGACTGGCCCTTCAACCATTTGCC	ATGATCTTGACATGATCTTGACATGAT	1452	
Db	1273	CTTGGACTGGCCCTTCAACCATTTGCC	ATGATCTTGACATGATCTTGACATGAT	1332	
Qy	1453	GGAGAAAGGAAACATGTGTAAAAAGT	CCGAGGGCAACATCATGTCCCTACATTTGGCAGGA	1512	
Db	1333	GGAGAAAGGAAACATGTGTAAAAAGT	CCGAGGGCAACATCATGTCCCTACATTTGGCAGGA	1392	
Qy	1513	CGCAATGAGTCTTCTCTCTGTCA	CCCTGCAGCCGCGACGATCTTACCAAAATTTCTAAG	1572	
Db	1393	CGCAATGAGTCTTCTCTCTGTCA	CCCTGCAGCCGCGACGATCTTACCAAAATTTCTAAG	1452	
Qy	1573	ACCGCTCAGCTATCTGCTTGCATCAG	CCAAAGCCTGTGAAGGAATCAAGTATCCT	1632	
Db	1453	ACCGCTCAGCTATCTGCTTGCATCAG	CCAAAGCCTGTGAAGGAATCAAGTATCCT	1512	
Qy	1633	GAGAAATTTGCGAGGAAATTAATGA	GCAACACACAGTGCAGTTCGAGAG	1692	
Db	1513	GAGAAATTTGCGAGGAAATTAATGA	GCAACACACAGTGCAGTTCGAGAG	1572	
Qy	1693	AAAGCCAAAGCTCTGCAAGCTTGA	AAAGGACATCTGTAAAGCCCTGTGGTGCAT	1752	
Db	1573	AAAGCCAAAGCTCTGCAAGCTTGA	AAAGGACATCTGTAAAGCCCTGTGGTGCAT	1632	
Qy	1753	CGATTTGGAAGAAATGTGAGACTTAA	TTTATGCGACGACAGAGGACAAATTTGTGGG	1812	
Db	1633	CGATTTGGAAGAAATGTGAGACTTAA	TTTATGCGACGACAGAGGACAAATTTGTGGG	1692	
Qy	1813	CATGACATGTGTGTCGGGGAGGACA	GTGTGTAATATGTGATGAAGCCCAAGCCC	1872	
Db	1693	CATGACATGTGTGTCGGGGAGGACA	GTGTGTAATATGTGATGAAGCCCAAGCCC	1752	
Qy	1873	ACCATGCGCATCTGTGTGGA	CTGTCTTTGGTCCC	CATGTCAGAGACTTGGAGGG	1932
Db	1753	ACCATGCGCATCTGTGTGGA	CTGTCTTTGGTCCC	CATGTCAGAGACTTGGAGGG	1812



QY	1039	TTGATCTTGGCAAGAGATATAAGCTTGTCTTAAGGCAATAGCGCTCTCTTAAGGCTC	1098
Db	793	TTCACTCTGGCAAGAGATATAAGCTTGTCTTAAGGCAATAGCGCTCTCTTAAGGCTC	852
QY	1099	CATAGAAATGAAAGACTGAACTGGAAGACTTGTGTGTGTGTCGACAAAAAGATGATGCA	1158
Db	853	CATTAAATGAAAGACTGAACTGGAAGACTTGTGTGTGTGTCGACAAAAAGATGATGCA	912
QY	1159	AAACATGGCCATGAAATATCAACACTTACGTGCTCAGATATCTCAATGATATCTGCT	1218
Db	913	AAACATGGCCATGAAATATCAACACTTACGTGCTCAGATATCTCAATGATATCTGCT	972
QY	1219	TTATTTCAAAA-----	1229
Db	973	TTATTTCAAAAAGATGAAACAATAGAGAAACAATCAATTGCATTTGATGCTGATTCCTT	1032
QY	1230	-----	1229
Db	1033	CTTAGAAGATGAACACCCAGAGACTGCTGATTAAGTCAACAGCAAGACCAACCTTAAGTAC	1092
QY	1230	-----TGATTTGATGGGAAAGATGGGACTCGTCATGACCAAGCATC	1272
Db	1093	TTCTGCAAGTGGCAAGCTGGATTTGATGGGAAAGATGGGACTCGTCATGACCAAGCATC	1152
QY	1273	TTACTGACTGGCTCTGGATATATGTTCTCTGGAAGATGAGCCCTGTGACACTTTGGGATTT	1332
Db	1153	TTACTGACTGGCTCTGGATATATGTTCTCTGGAAGATGAGCCCTGTGACACTTTGGGATTT	1212
QY	1333	GCACCCATTAAGTGAAGATGTGTAAATATGCACTGTCAGATTAAGAAGATACAGGT	1392
Db	1213	GCACCCATTAAGTGAAGATGTGTAAATATGCACTGTCAGATTAAGAAGATACAGGT	1272
QY	1393	CTTGGACTGGCCCTTACCACTTGGCCATGAGTCTGGACACAACCTTGGCATGATTCATGAT	1452
Db	1273	CTTGGACTGGCCCTTACCACTTGGCCATGAGTCTGGACACAACCTTGGCATGATTCATGAT	1332
QY	1453	GGAGAAAGGGAACATGTGTAAAAAGTCCAGAGGCAACATATGTCCCTACATTGGCAGGA	1512
Db	1333	GGAGAAAGGGAACATGTGTAAAAAGTCCAGAGGCAACATATGTCCCTACATTGGCAGGA	1392
QY	1513	GGCAATGAGTCTTCCCTGGTCAACCCTGACAGCCGCGCATATCTACAATAATTCCTAAG	1572
Db	1393	GGCAATGAGTCTTCCCTGGTCAACCCTGACAGCCGCGCATATCTACAATAATTCCTAAG	1452
QY	1573	ACCGCTCAAGCTATCTGCTTGTCTGATCAGCCAAAGCCTGTGAAGAAATACAAGTATCT	1632
Db	1453	ACCGCTCAAGCTATCTGCTTGTCTGATCAGCCAAAGCCTGTGAAGAAATACAAGTATCT	1512
QY	1633	GAGAAATTTGCCAGAGAAATTAATATGATCAAAACAAGTCAAGTGCAGATTCGAGAG	1692
Db	1513	GAGAAATTTGCCAGAGAAATTAATATGATCAAAACAAGTCAAGTGCAGATTCGAGAG	1572
QY	1693	AAAGCCAAGCTCTGCATGCTGAACTTTAAAAAGCACTGTGAAGCCCTGTGTGGCAT	1752
Db	1573	AAAGCCAAGCTCTGCATGCTGAACTTTAAAAAGCACTGTGAAGCCCTGTGTGGCAT	1632
QY	1753	CGTATTTGGAAGAAATGTGAGACTAAATTTATGCAAGCAGAGCAAGACAAATTTGTGG	1812
Db	1633	CGTATTTGGAAGAAATGTGAGACTAAATTTATGCAAGCAGAGCAAGACCAATTTGTGG	1692
QY	1813	CATGACATGTGTGCTCGGGAGAGACAGTGTGTGAATATGTGTGAAGGCCCCAGGCC	1872
Db	1693	CATGACATGTGTGCTCGGGAGAGACAGTGTGTGAATATGTGTGAAGGCCCCAGGCC	1752
QY	1873	ACCCATGGCCACTGTGCTGGACTGTCTTCTTGTGTCCCATATGCTCCAGACCTGTGGAGG	1932
Db	1753	ACCCATGGCCACTGTGCTGGACTGTCTTCTTGTGTCCCATATGCTCCAGACCTGTGGAGG	1812
QY	1933	GGAGTATCTCATAGAGAGTGCCTCTGCAACAACCCCAAGCCATCGATGAGGGGAATTC	1992
Db	1813	GGAGTATCTCATAGAGAGTGCCTCTGCAACAACCCCAAGCCATCGATGAGGGGAATTC	1872
QY	1993	TGTAGGGCTCCACTTCGCACTTCGAAAGCTTGTGCAACAGTCAAGAAATGTCCCCGGGACGT	2052

Db	1873	TGTGAGGGCTTCACCTCGCACCCTTGAAGCTCTGCACAGTCAGAAATGTCCCGGGACAGT	1932
Qy	2053	GTTCACATTCGCTGCTGCTCACTGTGTGCGGACCAACAGACGATTCAGAGGGCGGCAC	2112
Db	1993	GTTCAGCTTCGGTGTGCTCAGTGTGTGCCAGCAACAGCAGACGATTCAGAGGGCGGCAC	1992
Qy	2113	TACAAAGTGAAGCCTTACATCACTAGTAGAAGATCAGACCTTATGCAAACTCTATGTATC	2172
Db	1993	TACAAAGTGAAGCCTTACATCACTAGTAGAAGATCAGACCTTATGCAAACTCTATGTATC	2052
Qy	2173	GCAGAGGATTTGATTTCTTCTTCTTCTTGTGCAATAAGTCAAAAGTGGGACCTCCATGC	2232
Db	2053	GCAGAGGATTTGATTTCTTCTTCTTCTTGTGCAATAAGTCAAAAGTGGGACCTCCATGC	2112
Qy	2233	TCGGAGGATAGCCGTAATGTTTGTATAGATGGATATGTGAGAGGTTGATGTGACAT	2292
Db	2113	TCGGAGGATAGCCGTAATGTTTGTATAGATGGATATGTGAGAGGTTGATGTGACAT	2172
Qy	2293	GTCTTGGATCTGATGCTGTGTGAAGACGTCTGTGGGGTGTGTAAACGGGAATTACTCAGCC	2352
Db	2173	GTCTTGGATCTGATGCTGTGTGAAGACGTCTGTGGGGTGTGTAAACGGGAATTACTCAGCC	2232
Qy	2353	TGCACAGATTCACAGGGGTCTCTACACCAAGACACACACCAACAGTATTAACAATG	2412
Db	2233	TGCACAGATTCACAGGGGTCTCTACACCAAGACACACACCAACAGTATTAACAATG	2292
Qy	2413	GTCAACCATTCCTTGTGAGCCCGGAGATTCGCACTATGCAAAATGAACGTCTCACTCC	2472
Db	2293	GTCAACCATTCCTTGTGAGCCCGGAGATTCGCACTATGCAAAATGAACGTCTCACTCC	2352
Qy	2473	TACATTTCTGTGCGCAATGCTCTCAGAAAGTACTACTGAATGGGCACTGACCCGTGAC	2532
Db	2353	TACATTTCTGTGCGCAATGCTCTCAGAAAGTACTACTGAATGGGCACTGACCCGTGAC	2412
Qy	2533	TGGCCCGGCGGTACAAATTTTGGGGCATTACTTTGCACTACAGACGCTCTATAAGAG	2592
Db	2413	TGGCCCGGCGGTACAAATTTTGGGGCATTACTTTGCACTACAGACGCTCTATAAGAG	2472
Qy	2593	CCCGAGAACTTAATCGCTACTGACCAACCAACGACACTGATTTGAGAGCTGCTGTT	2652
Db	2473	CCCGAGAACTTAATCGCTACTGACCAACCAACGACACTGATTTGAGAGCTGCTGTT	2532
Qy	2653	CAGGGAAGAAACCCGGGTGTTCTGTGGGAATATCTCATGCTCGCTTGGGGACCGAAGAG	2712
Db	2533	CAGGGAAGAAACCCGGGTGTTCTGTGGGAATATCTCATGCTCGCTTGGGGACCGAAGAG	2592
Qy	2713	CAGCCCTTGTGCGCAGCCCACTACACTTTGGGCCATGCTGGGCTTGTAGTGTCCGTGTC	2772
Db	2593	CAGCCCTTGTGCGCAGCCCACTACACTTTGGGCCATGCTGGGCTTGTAGTGTCCGTGTC	2652
Qy	2773	TGCGGAGGGGG 2783	
Db	2653	TGCGGAGGGGG 2663	
RESULT 6			
US-10-236-616-1			
; Sequence 1, Application US/10296616			
; Publication No. US20030129658A1			
; GENERAL INFORMATION:			
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.			
; TITLE OF INVENTION: No. US20030129658A1el protease			
; FILE REFERENCE: Y0132PCT-664			
; CURRENT FILING DATE: 2002-11-26			
; PRIOR FILING DATE: 2000-12-25			
; NUMBER OF SEQ ID NOS: 26			
; SEQ ID NO 1			
; LENGTH: 3675			
; TYPE: DNA			
; ORGANISM: Homo sapiens			

FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1) .. (3675)  
US-10-296-616-1

Query Match 64.8%; Score 1874.6; DB 15; Length 3675;

Best Local Similarity 84.4%; Pred. No. 0;  
Matches 2287; Conservative 0; Mismatches 179; Indels 245; Gaps 6;

```
QY 202 GCAGGCACTGCGTGCATGAGAACCCGACGCGCAGCGCTGGAGCCCGACGCTCC 261
DB 69 GCAGGCACTGCGTGCATGAGAACCCGACGCGCAGCGCTGGAGCCCGACGCTCC 128
QY 262 GCGTCTCTCTCAACCGCGGAGCGCGCGCTGATGAAAGCGCGGACATGATGAA 321
DB 129 GCGTCTCTCTCAACCGCGGAGCGCGCGCTGATGAAAGCGCGGACATGATGAA 175
QY 322 GGTGAAACATGTTCTGACAACTAACAGAAACGAAACCAACACTGATGTT 381
DB 176 ----- 175
QY 382 CTCACATATATGACCTGTCTCTGCTACAGAGTTGACACAGGCGCATTAAGTTC 441
DB 176 -----AATATACCTGGTCTCTGCTTAAGAGTTGACACAGGCGCATTAAGTTC 228
QY 442 CATGAATCATGACCATCAGCGCGGAGAAAGCAGTGGCGGTTCGAGTTGATCT 501
DB 229 CATGAATCATGACCATCAGCGCGGAGAAAGCAGTGGCGGTTCGAGTTGATCT 288
QY 502 CTCACCTTGCGGTGAAAGGCCCGACGACGCTTCACATGATCTAGAGACTTCAG 561
DB 289 CTCACCTTGCGGTGAAAGGCCCGACGACGCTTCACATGATCTAGAGACTTCAG 348
QY 562 AGCTAGTGGCTCTGCTTTATTTGACAGCCTTGGAAAGACAGGCACTAAGTCTG 621
DB 349 AGCTAGTGGCTCTGCTTTATTTGACAGCCTTGGAAAGACAGGCACTAAGTCTG 408
QY 622 CAGACTTTACCGGACAGAGACTTCTGTTTATCAAGGCTCTTTGGATGACACAGAA 681
DB 409 CAGACTTTACCGGACAGAGACTTCTGTTTATCAAGGCTCTTTGGATGACACAGAA 468
QY 682 TGSCATCGATGAGAGAAATTCTGTAGGCGCTCCACTGCACTGAAAGCTCTGAA 741
DB 469 TCTCTCA-----GTGGCCCTTTCAACCTGCGCAAGGCTTGTC 504
QY 742 AGTCAGAAATGTCCCGGACAGTGTGAATTCGCTGCTCAGTGTCCGACGACAA 801
DB 505 GGCATGATACGAACAGAAAGGACGATTAATCTTAAGGCACTTCTTACACCTCTCA 564
QY 802 AGCAGACGATTCAGAGGCGGACCTACAAAGTGG--AAAGCTTAAGTCAAGTGA 859
DB 565 TGGAAACTGGGAGAGCTGCCAAGGACGCTGCCATCCACGTAACGTACGTAAGA 624
QY 860 ACTTATGCAAACTCTAAGTATGCAAGAAAGATTGATTTCTTTCTTTGTCAAA 919
DB 625 ACAGAGACCCCATGCTCTGCGGACGAGTGAAGTCTGTGACCTC-----AA 672
QY 920 AAGTCAAGATGAGGACTCCATGCTCGAAGATAGCCGTAATGTTGTATGATGG 979
DB 673 ACATGGAGAGCTGGACATCAACCTTGACAGCAGGACCTTGCGCTGGGACCTG 732
QY 980 GTGAGCTCAGTGTGTCTCAATCTGCG--GCAATGCCCCAGCTTCCAGAAAGCT 1038
DB 733 AAGCAGCATTTTGTGAAAGACGCAAGAAATACATGCCCGACCTCCAGAGAA 792
QY 1039 TTTCATCTTGCGAGATGATTAAGTCTTGCTTAAGGCTCTCTTTGAGGCTCC 1098
DB 793 TTTCATCTTGCGAGATGATTAAGTCTTGCTTAAGGCTCTCTTTGAGGCTCC 852
QY 1099 CATAGAAATGAAAGAACTGAACGTGAGACCTTGGTGTGTGACAAAAGATGAT 1158
DB 853 CATAGAAATGAAAGAACTGAACGTGAGACCTTGGTGTGTGACAAAAGATGAT 912
```

```
QY 1159 AACCATGGCCATGAATAATATCAACCTTACGCTGTACAGATATCTCAACATG 1218
DB 913 AACCATGGCCATGAATAATATCAACCTTACGCTGTACAGATATCTCAACATG 972
QY 1219 TTAATCAAGA----- 1229
DB 973 TTAATCAAGAATGGAACATATAGAGAGAAACATCAACATTGCAATTGTAGTCT 1032
QY 1230 ----- 1229
DB 1033 CTAGAAAGATGAACACGACGAGACTGGTGAATTAAGTACACGACGACACCTTA 1092
QY 1230 -----TGATTAATGGGAAAGATGGGACTGTGTATGACACCGCATC 1272
DB 1093 TTCTGCACTGGTCACTGATTTGAATGGGAAAGATGGGACTGTGTATGACACCG 1152
QY 1273 TTAAGTCTGTCTGATATATGTTCTGTGAAAGAAATGAGCCCTGTGACACTTT 1332
DB 1153 TTAAGTCTGTCTGATATATGTTCTGTGAAAGAAATGAGCCCTGTGACACTTT 1212
QY 1333 GCACCCATTAAGTGAATGTATGTAATAATCGACCTGACGATTAATGAAGATAC 1392
DB 1213 GCACCCATTAAGTGAATGTATGTAATAATCGACCTGACGATTAATGAAGATAC 1272
QY 1393 CTTGGAATGAGCTTTACCACTTGTCCATGAGTCTGACACAACTTTGGCATGAT 1452
DB 1273 CTTGGAATGAGCTTTACCACTTGTCCATGAGTCTGACACAACTTTGGCATGAT 1332
QY 1453 GGAGAAAGGAAACATGTGTAAAGTCCGAGGCAACATCATGCTCCCTACATTTG 1512
DB 1333 GGAGAAAGGAAACATGTGTAAAGTCCGAGGCAACATCATGCTCCCTACATTTG 1392
QY 1513 CGCAATGAGTCTTCTCTGTGACCTGACCGCGCAGATATCAACAAATTTCTAAG 1572
DB 1393 CGCAATGAGTCTTCTCTGTGACCTGACCGCGCAGATATCAACAAATTTCTAAG 1452
QY 1573 ACCGCTCAAGCTATCTGCTTGTGATGACGCAAGAGCTGTGAAGAAATCAAG 1632
DB 1453 ACCGCTCAAGCTATCTGCTTGTGATGACGCAAGAGCTGTGAAGAAATCAAG 1512
QY 1633 GAGAAATGCGCAGAGAAATTAATATGATGCAACACAGTGTGAGTGGAGAG 1692
DB 1513 GAGAAATGCGCAGAGAAATTAATATGATGCAACACAGTGTGAGTGGAGAG 1572
QY 1693 AAAGCAAGCTCTGCATGCTGGAATTTAAAGACATCTGTAAAGCCCTGTGTC 1752
DB 1573 AAAGCAAGCTCTGCATGCTGGAATTTAAAGACATCTGTAAAGCCCTGTGTC 1632
QY 1753 CGTATTGGAAGAAATGTGAAGCTAAATTTATGCGACGACGAAAGGCACAAT 1812
DB 1633 CGTATTGGAAGAAATGTGAAGCTAAATTTATGCGACGACGAAAGGCACAAT 1692
QY 1813 CATGACATGTGGTGGCGGAGAGACAGTGTGAAATTAATGATGAAGAGGCCCAAG 1872
DB 1693 CATGACATGTGGTGGCGGAGAGACAGTGTGAAATTAATGATGAAGAGGCCCAAG 1752
QY 1873 ACCCATGGCCATGTGTGGAATGTTCTTTGTTGCCATGTCTCGAGACCTGCGAG 1932
DB 1753 ACCCATGGCCATGTGTGGAATGTTCTTTGTTGCCATGTCTCGAGACCTGCGAG 1812
QY 1933 GAGATATCTCATAGAGAGTGGCTCTGACCAACCCCAAGCCATGCGATGAGAGGA 1992
DB 1813 GAGATATCTCATAGAGAGTGGCTCTGACCAACCCCAAGCCATGCGATGAGAGGA 1872
QY 1993 TGTGAGGCTCAACTGCACTCTGAAGCTCTGCAACAGTCAAGAAATGTCCCGGAG 2052
DB 1873 TGTGAGGCTCAACTGCACTCTGAAGCTCTGCAACAGTCAAGAAATGTCCCGGAG 1932
QY 2053 GTTGACTTCCGTGCTCTCACTGTGTGCGAGCAACAGCAGACGATTTGAGAGGG 2112
DB 1933 GTTGACTTCCGTGCTCTCACTGTGTGCGAGCAACAGCAGACGATTTGAGAGGG 1992
QY 2113 TACAAAGTGAAGCCTTACACTCAAGTGAAGATCAGGACTTAATGCAACTTACT 2172
```





QY 1219 TTAATCAGAA----- 1229  
Db 973 TTAATCAAAAGATGGAACAAATAGAGGAAACATCAATTGCAATTGAGTCTGATTTCTT 1032  
QY 1230 ----- 1229  
Db 1033 CTGAAAGATGAAACGACGAGCTGTGATTAAGTCAACGACGAGAACACACTTAACTAGAC 1092  
QY 1230 -----TGAATTGATGGGAAAGATGGGACTGCTGATGACCAAGCCATC 1272  
Db 1093 TTTCGCACTGAGCTGTGATTTGATGGGAAAGATGGGACTCGTCAATGACCAAGCCATC 1152  
QY 1273 TTAATCACTGTGTGATTAATATTTCTGTGAAAGAAAGAGCCCTGTGACACTTTGGGATTT 1332  
Db 1153 TTAATCACTGTGTGATTAATATTTCTGTGAAAGAAAGAGCCCTGTGACACTTTGGGATTT 1212  
QY 1333 GCACCATTAAGTGAATGTGTAGTAATAATCGAGCTGACAGATTAATGAAAGATACAGGT 1392  
Db 1213 GCACCATTAAGTGAATGTGTAGTAATAATCGAGCTGACAGATTAATGAAAGATACAGGT 1272  
QY 1393 CTGTGACTGGCTTTCACCAATTTGCAATGAGTCTGACACAACTTTGGCATGATTCATGAT 1452  
Db 1273 CTGTGACTGGCTTTCACCAATTTGCAATGAGTCTGACACAACTTTGGCATGATTCATGAT 1332  
QY 1453 GGAAGAGGAAACATGTGTAAAGTCCGAGGGAACATCATGTCCCTACATTTGGAGGA 1512  
Db 1333 GGAAGAGGAAACATGTGTAAAGTCCGAGGGAACATCATGTCCCTACATTTGGAGGA 1392  
QY 1513 CGCAATGAGTCTTCTCTGTGTCACTGAGCCGCAAGTATCTACACAAATTTCTAAGC 1572  
Db 1393 CGCAATGAGTCTTCTCTGTGTCACTGAGCCGCAAGTATCTACACAAATTTCTAAGC 1452  
QY 1573 ACCGCTCAAGCTATCTGCTTCTGTATCAGCCAAAGCTGTGAAAGATACAAATTCCT 1632  
Db 1453 ACCGCTCAAGCTATCTGCTTCTGTATCAGCCAAAGCTGTGAAAGATACAAATTCCT 1512  
QY 1633 GGAATTTGCGCAGAGAAATTAATATGAAACACACAGTGGCAATGGGAGTTCCGAGAG 1692  
Db 1513 GGAATTTGCGCAGAGAAATTAATATGAAACACACAGTGGCAATGGGAGTTCCGAGAG 1572  
QY 1693 AAAGCAAGCTCTGATGCTGACTTTAAAGAGATCTGTAAAGCCCTGTGTGCTCAT 1752  
Db 1573 AAAGCAAGCTCTGATGCTGACTTTAAAGAGATCTGTAAAGCCCTGTGTGCTCAT 1632  
QY 1753 CGTATTGGAAGAAATGTGACTAAATTTATCCAGCAGAGAAAGCAAAATTTGTGGG 1812  
Db 1633 CGTATTGGAAGAAATGTGACTAAATTTATCCAGCAGAGAAAGCAAAATTTGTGGG 1692  
QY 1813 CATGACATGTGTGCGGGGAGGACAGTGTGAAATATGTGATGAAGGCCCAAGCCC 1872  
Db 1693 CATGACATGTGTGCGGGGAGGACAGTGTGAAATATGTGATGAAGGCCCAAGCCC 1752  
QY 1873 ACCCATGGCACTGTGCGAGCTGTCTTGTGCTCCCATGCTCCAGACCTGCGAGAG 1932  
Db 1753 ACCCATGGCACTGTGCGAGCTGTCTTGTGCTCCCATGCTCCAGACCTGCGAGAG 1812  
QY 1933 GGAATATCTCATATGAGTGTGCTCTGCAACCAACCCCAAGCCATGCGATGGAAGGAAATT 1992  
Db 1813 GGAATATCTCATATGAGTGTGCTCTGCAACCAACCCCAAGCCATGCGATGGAAGGAAATT 1872  
QY 1993 TGTGAGGGGCTCCACTGGCACTGTGAGCTGTGCAAGTCAGAAAGTATCCCGGAGCACT 2052  
Db 1873 TGTGAGGGGCTCCACTGGCACTGTGAGCTGTGCAAGTCAGAAAGTATCCCGGAGCACT 1932  
QY 2053 GTTGAATTCCTGCTGCTGCTGAGTGTGCGGAGCAACAGAGAGATTCAGAGGGCGGAC 2112  
Db 1933 GTTGAATTCCTGCTGCTGCTGAGTGTGCGGAGCAACAGAGAGATTCAGAGGGCGGAC 1992  
QY 2113 TACAGTGAAGCTTTACACTCAAGTGAAGATCAGAGCTTATGCAAACTTACTGTATC 2172  
Db 1993 TACAGTGAAGCTTTACACTCAAGTGAAGATCAGAGCTTATGCAAACTTACTGTATC 2052  
QY 2173 GGAAGAGATTTGATTTCTTTCTTTGTCAAAATAAAGTCAAAAGATGGGACTCATGC 2232

Db 2053 GGAAGAGATTTGATTTCTTTCTTTGTCAAAATAAAGTCAAAAGATGGGACTCATGC 2112  
QY 2233 TCGAGAGATAGCCGTAATGTTGTATAGTGGGATATGAGAGATTGATGTGCAAT 2292  
Db 2113 TCGAGAGATAGCCGTAATGTTGTATAGTGGGATATGAGAGATTGATGTGCAAT 2172  
QY 2293 GTCTTGTGATGTGATGCTGTGTGAAGACGTCTGTGGGGTGTGTAAAGGAAATTAATCAGCC 2352  
Db 2173 GTCTTGTGATGTGATGCTGTGTGAAGACGTCTGTGGGGTGTGTAAAGGAAATTAATCAGCC 2232  
QY 2353 TGCAGATTCACAGGGGTCTCTACACCAAGCACCAACCAACAGATTAATCAGATG 2412  
Db 2233 TGCAGATTCACAGGGGTCTCTACACCAAGCACCAACCAACAGATTAATCAGATG 2292  
QY 2413 GTCAACATTCCTTCTGAGAGCCGAGATATCCGATCTATGAATGAACGTCTACCTCC 2472  
Db 2293 GTCAACATTCCTTCTGAGAGCCGAGATATCCGATCTATGAATGAACGTCTACCTCC 2352  
QY 2473 TACATTTCTGTGCGCAATGCTCTCAGAAAGTACTACCTGAATGGGCACTGACCGGTGAC 2532  
Db 2353 TACATTTCTGTGCGCAATGCTCTCAGAAAGTACTACCTGAATGGGCACTGACCGGTGAC 2412  
QY 2533 TGGCCCGCGGTACAAATTTTCCGGGCACTACTTTCGATCAGACGGTCTATATGAG 2592  
Db 2413 TGGCCCGCGGTACAAATTTTCCGGGCACTACTTTCGATCAGACGGTCTATATGAG 2472  
QY 2593 CCCGAACTTAATCGTACTGACCAACCAACGAGACATGATTTGTGAGCTGTGTT 2652  
Db 2473 CCCGAACTTAATCGTACTGACCAACCAACGAGACATGATTTGTGAGCTGTGTT 2532  
QY 2653 CAGGGAAGAACCCGGGTGTGCTGTGGAATATCTCATATGCTGCTTGGGAGCCGAGAG 2712  
Db 2533 CAGGGAAGAACCCGGGTGTGCTGTGGAATATCTCATATGCTGCTTGGGAGCCGAGAG 2592  
QY 2713 CAGCCCTGCGCCAGCCGAGCTACCTTGGGCAATGCTGAGTGTGCTGAGTGTGCTG 2772  
Db 2593 CAGCCCTGCGCCAGCCGAGCTACCTTGGGCAATGCTGAGTGTGCTGAGTGTGCTG 2652  
QY 2773 TCGGAGGGGG 2783  
Db 2653 TCGGAGGGGG 2663

RESULT 8  
US-10-217-774-5  
; Sequence 5, Application US/10217774  
; Publication No. US20020193583A1  
; GENERAL INFORMATION:  
; APPLICANT: Fiddie, Carl Johan  
; APPLICANT: Hibun, Erin  
; TITLE OF INVENTION: No. US20020193583A1e1 Human Proteases and Polynucleotides Encoding  
; FILE REFERENCE: LEX-0219-USA  
; CURRENT FILING DATE: 2002-08-12  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: US 60/225,852  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-217-774-5

Query Match 64.8%; Score 1874.6; DB 13; Length 4042;  
Best Local Similarity 84.4%; Pred. No. 0;  
Matches 2287; Conservative 0; Mismatches 179; Indels 245; Gaps 6;  
QY 202 GCAAGCACCTGCTGCGCATGGACCCGACGGCAGCGCTGTGGAGCCGAGCGTCCC 261

|||||  
Db 167 GCAGGCACTGCGTGCATGGGACCCGACGGCAGCGCTGGAGGCCGCGCTGCC 226  
Qy 262 GGGTCTCTCCACCCGCGAGCGCGCGCTGGATGGAAAGAGGGGGGCAATGATGAA 321  
Db 227 GGGTCTCTCCACCCGCGAGCGCGCGCTGGATGGAAAGAGGGCG----- 273  
Qy 322 GCTGAAACCATCGTTCTCAGCAACTTAACAGAAACAGAAACCAACACTGATGTT 381  
Db 274 ----- 273  
Qy 382 CTCACCTCAATGACCTGGTCTCTGCCCTACGAGTTGACCAAGGGCGATTAAGTGTCC 441  
Db 274 -----AATATGACCTGGTCTCTGCCCTACGAGTTGACCAAGGGCGATTAAGTGTCC 326  
Qy 442 CATGAAATATGACATCAGCGCGCGAGAAAGAGCGTGGCCCTGTCGAGGTGAGTCT 501  
Db 327 CATGAAATATGACATCAGCGCGCGAGAAAGAGCGTGGCCCTGTCGAGGTGAGTCT 386  
Qy 502 CTTCACTTCGCGTGAAGGCGCCGAGCAAGCTTCAACATGATCTGAGGACTTCAGC 561  
Db 387 CTTCACTTCGCGTGAAGGCGCTCAGGCAAGCTTCAAGTGAATCTGAGGACTTCAGC 446  
Qy 562 AGCTTAGTGGCTCTGGCTTATTTATGTGACAGCGTTGGAAAGACAGGCACTAAGTCTGTG 621  
Db 447 AGCTTAGTGGCTCTGGCTTATTTATGTGACAGCGTTGGAAAGACAGGCACTAAGTCTGTG 506  
Qy 622 CAGACTTACCGGCAAGAGACTTCTGTTTATCAAGAGCTCTTTGGGATCAACAGAAAC 681  
Db 507 CAGACTTACCGGCAAGAGACTTCTGTTTATCAAGAGCTCTTTGGGATCAACAGAAAC 566  
Qy 682 TCGCCATCGCATGAGAGGAATCTGTGAGGGCTCCACTGCACTGCAAGCTCTGCAAC 741  
Db 567 TCTCTCA-----GTGGCCCTTTCAACCTTGCCAGGCTTGTCA 602  
Qy 742 AGTCAAAATGTCCCGGGAAGAGTGTGACTTCGCTGCTCAGTGTGCCAGCAAC 801  
Db 603 GGCATGATACGAACAGAGAGGAGATTACTTCTTAAGGCCACTTCTTCAACACTCTCA 662  
Qy 802 AGCAGACGATTCAGAGGGCGGCACTACAAATGG--AAGCTTACACTCAAGTGAAGCG 859  
Db 663 TGGAACTCGGAGAGCTGCGCAAGGCAAGCTGCAATCCACGTACTGTACAGAGATCC 722  
Qy 860 ACTTATGCAAACTCTACTGTATGCGAAGAGATTTGATTTCTCTTTTCTTTGTCAATA 919  
Db 723 ACAGAGCCCATGCTCTGGGGCAAGTGAAGTCTGTGACTC-----AAG 770  
Qy 920 AAGTCAAAATGGGACTCCATGCTCGAAGATAGCCGTAAATGTTGTATAGATGGATAT 979  
Db 771 ACATGGGAGCTGGCATCAACCCCTGCACAGCAGGACCTTGCGCTGGGACTGCCACA 830  
Qy 980 GTGAGCTCAGTGTGTGTCACTGTGC--GCATAGCCCCAGCTCCCAAGAAACCTC 1038  
Db 831 AAGCAGCATTTTCTGTGAAGACCGAAGAAATACATCCCCAGGCTCCCAAGAAACCTC 890  
Qy 1039 TTTCATCTTGCAGATAGTATTAAGTCTTGCTTACGGGATTAAGGCTCTCTTGAAGTTC 1098  
Db 891 TTTCATCTTGCAGATAGTATTAAGTCTTGCTTACGGGATTAAGGCTCTCTTGAAGTTC 950  
Qy 1099 CATAGAAATGAAGACTGAACGTGAGACCTTGTGGTGTGACAAAAGATGATGCA 1158  
Db 951 CATAGAAATGAAGACTGAACGTGAGACCTTGTGGTGTGACAAAAGATGATGCA 1010  
Qy 1159 AACCATGGCCATGAAATATACCACTTACGTGTCTACGATATCAACATGATGTGCT 1218  
Db 1011 AACCATGGCCATGAAATATACCACTTACGTGTCTACGATATCAACATGATGTGCT 1070  
Qy 1219 TTAATCAAGA----- 1229  
Db 1071 TTAATCAAGA----- 1130  
Qy 1230 ----- 1229

Db 1131 CTAGAAATGAAACAGCAGAGACTGGTGAATAGTCAACAGCAGACCACTTAATGATC 1190  
Qy 1230 -----TGAATTGATGGGAAAGATGGGACTGTGATGACCAAGCATC 1272  
Db 1191 TTCTGCACTGGCAGCTGTGATTTGATGGGAAAGATGGGACTGTGATGACCAAGCATC 1250  
Qy 1273 TTAATGACTGGTCTGGATATTAATGTTCTTGAAAGAAATGAGCCCTGTGACCTTTGGATTT 1332  
Db 1251 TTAATGACTGGTCTGGATATTAATGTTCTTGAAAGAAATGAGCCCTGTGACCTTTGGATTT 1310  
Qy 1333 GCAACCATTAAGTGAATGTGTGTAATATTCGAGCTGACAGATTAATTAAGTACAGT 1392  
Db 1311 GCAACCATTAAGTGAATGTGTGTAATATTCGAGCTGACAGATTAATTAAGTACAGT 1370  
Qy 1393 CTTGAGCTGGCTTCAACATTCGCCATGAGTGTGACCAACTTTGGCATGATCATGAT 1452  
Db 1371 CTTGAGCTGGCTTCAACATTCGCCATGAGTGTGACCAACTTTGGCATGATCATGAT 1430  
Qy 1453 GGAGAAAGGAAATGTGTAAAAAGTCCAGAGGCAACATCATGTCCCTTACATTGGCAGGA 1512  
Db 1431 GGAGAAAGGAAATGTGTAAAAAGTCCAGAGGCAACATCATGTCCCTTACATTGGCAGGA 1490  
Qy 1513 CGCATGAGTCTTCTCTGTGTCACTTGACAGCCGCAAGTATCTACAAATTTCTAAGC 1572  
Db 1491 CGCATGAGTCTTCTCTGTGTCACTTGACAGCCGCAAGTATCTACAAATTTCTAAGC 1550  
Qy 1573 ACCGCTCAAGCTTATCTGCTTGTGTGACAGCAAGCCGTGTGAAGGAAATACAATGCTCT 1632  
Db 1551 ACCGCTCAAGCTTATCTGCTTGTGTGACAGCAAGCCGTGTGAAGGAAATACAATGCTCT 1610  
Qy 1633 GAGAAATTCGCAAGAAATTAATGATGCAACACACAGTGCAGAGTGGCATTCGAGAG 1692  
Db 1611 GAGAAATTCGCAAGAAATTAATGATGCAACACACAGTGCAGAGTGGCATTCGAGAG 1670  
Qy 1693 AAAGCAGACTCTGCATGCTGTGACTTTAAAGAGACATCTGTAAAGCCCTGTGTGCTCAT 1752  
Db 1671 AAAGCAGACTCTGCATGCTGTGACTTTAAAGAGACATCTGTAAAGCCCTGTGTGCTCAT 1730  
Qy 1753 CGTATGGAAGGAAATGTGAGACTAAATTTATGCGCAGCAGAGAGGCAAAATTTGTGG 1812  
Db 1731 CGTATGGAAGGAAATGTGAGACTAAATTTATGCGCAGCAGAGAGGCAAAATTTGTGG 1790  
Qy 1813 CATGACATGTGTGCGGGAGAGACAGTGTGAAATATGATGATGAAGGCCCAAGCCC 1872  
Db 1791 CATGACATGTGTGCGGGAGAGACAGTGTGAAATATGATGATGAAGGCCCAAGCCC 1850  
Qy 1873 ACCCATGGCCATGGTGGGACTGTTCTTGTGCTCCCATGCTCCAGACCTGCGGAGGG 1932  
Db 1851 ACCCATGGCCATGGTGGGACTGTTCTTGTGCTCCCATGCTCCAGACCTGCGGAGGG 1910  
Qy 1933 GGAATATCTCATAGAGGTGCGCTGACCAACCCCAAGCCATGCGATGGAAGGAAGTTC 1992  
Db 1911 GGAATATCTCATAGAGGTGCGCTGACCAACCCCAAGCCATGCGATGGAAGGAAGTTC 1970  
Qy 1993 TGTGAGGGCTCACTGCACTGCAAGCTCTGCAACAGTCAAGAAATGTCCCGGGAAGT 2052  
Db 1971 TGTGAGGGCTCACTGCACTGCAAGCTCTGCAACAGTCAAGAAATGTCCCGGGAAGT 2030  
Qy 2053 GTTGACTTCGTGCTGCTCAGTGTGCGAGCAACAAGCAAGACGATTCAGAGGGCGGAC 2112  
Db 2031 GTTGACTTCGTGCTGCTCAGTGTGCGAGCAACAAGCAAGACGATTCAGAGGGCGGAC 2090  
Qy 2113 TACAGTGAAGCCCTTACACTCAAGTGAAGATCGAGACTTATGCAAACTTACTGTATC 2172  
Db 2091 TACAGTGAAGCCCTTACACTCAAGTGAAGATCGAGACTTATGCAAACTTACTGTATC 2150  
Qy 2173 GCAGAGGATTTGATTTCTTCTTTCTTGTCAAAATTAAGTCAAAAGATGGGACTCCATGC 2232  
Db 2151 GCAGAGGATTTGATTTCTTCTTTCTTGTCAAAATTAAGTCAAAAGATGGGACTCCATGC 2210  
Qy 2233 TCGAGAGATAGCCGTATATGTTGTATAGATGGGATATGTGAGAGATGTGATGCAAT 2292  
Db 2211 TCGAGAGATAGCCGTATATGTTGTATAGATGGGATATGTGAGAGATGTGATGCAAT 2270

```
QY 2293 GTCTTGATCTGATCTGTTGAAGACGTCTGTGGGGTGTGTAACGGGAATTAATCAGCC 2352
    |||
    |||
    |||
Db 2271 GTCTTGATCTGATCTGTTGAAGACGTCTGTGGGGTGTGTAACGGGAATTAATCAGCC 2330
    |||
    |||
    |||
QY 2353 TGCAGGATTCAGAGGGGTCTCTACACCAAGACACACACCAAGATTAATCAAG 2412
    |||
    |||
    |||
Db 2331 TGCAGGATTCAGAGGGGTCTCTACACCAAGACACACCAAGATTAATCAAG 2390
    |||
    |||
    |||
QY 2413 GTACCAATTCCTTGTGAGCCCGAGATCCGATCTATGAATGAACGTCTTACTCC 2472
    |||
    |||
    |||
Db 2391 GTACCAATTCCTTGTGAGCCCGAGATCCGATCTATGAATGAACGTCTTACTCC 2450
    |||
    |||
    |||
QY 2473 TACATTTCTGTGGCAATGCTCTCAGAAAGTACTCTGAATGGGCACTGGACCTGGAC 2532
    |||
    |||
    |||
Db 2451 TACATTTCTGTGGCAATGCTCTCAGAAAGTACTCTGAATGGGCACTGGACCTGGAC 2510
    |||
    |||
    |||
QY 2533 TGGCCCGCGGATCAAAATTTTCGGGCACTTCTGACCTAGAGAGGCTTAAATGAG 2592
    |||
    |||
    |||
Db 2511 TGGCCCGCGGATCAAAATTTTCGGGCACTTCTGACCTAGAGAGGCTTAAATGAG 2570
    |||
    |||
    |||
QY 2593 CCCGAACTTAATGCTACTGAGCCACCAACGAGACACTGATGTGAGGCTGCTGTT 2652
    |||
    |||
    |||
Db 2571 CCCGAACTTAATGCTACTGAGCCACCAACGAGACACTGATGTGAGGCTGCTGTT 2630
    |||
    |||
    |||
QY 2653 CAGGGAAGAACCCGGGTGTGCTTGGGAATCTCATGCTGCTTGGGACCGAAG 2712
    |||
    |||
    |||
Db 2631 CAGGGAAGAACCCGGGTGTGCTTGGGAATCTCATGCTGCTTGGGACCGAAG 2690
    |||
    |||
    |||
QY 2713 CAGCCCTGCGCAGCCGAGCTACACTTGGGCACTGTGAGTGTCCGATCC 2772
    |||
    |||
    |||
Db 2691 CAGCCCTGCGCAGCCGAGCTACACTTGGGCACTGTGAGTGTCCGATCC 2750
    |||
    |||
    |||
QY 2773 TCGGAGGGGG 2783
    |||
    |||
    |||
Db 2751 TCGGAGGGGG 2761
    |||
    |||
    |||
RESULT 9
US-10-804-457-5
; Sequence 5, Application US/10804457
; Publication No. US2005006534A1
; GENERAL INFORMATION:
; APPLICANT: Fiddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: Novel Human Proteases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/10/804,457
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US/10/217,774
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/930,872
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4042
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-804-457-5

Query Match 64.8%; Score 1874.6; DB 21; Length 4042;
Best Local Similarity 84.4%; Pred. No. 0;
Matches 2287; Conservative 0; Mismatches 179; Indels 245; Gaps 6;
```

```
Db 227 GGTCTCTCTCACCAGGAGGCGCGGCTGTGAGAAAAGGCG----- 273
    |||
    |||
    |||
QY 322 GGTGAAAACCATGTTCTCAGAAACTAAACACAGAAACAGAAAACCAACATCTGATGTT 381
    |||
    |||
    |||
Db 274 ----- 273
    |||
    |||
    |||
QY 382 CTCACCTAATATGACCTTGGTCTGTGCTTACGAGGTTGACACAGAGGCGATTAAGTCTC 441
    |||
    |||
    |||
Db 274 -----AATATGACCTTGGTCTGTGCTTACGAGGTTGACACAGAGGCGATTAAGTCTC 326
    |||
    |||
    |||
QY 442 CATGAATATGACCAATCAGCGGGGAGAGAGAGAGGCGCGTCTCCAGGTTAGTCT 501
    |||
    |||
    |||
Db 327 CATGAATATGACCAATCAGCGGGGAGAGAGAGAGGCGCGTCTCCAGGTTAGTCT 386
    |||
    |||
    |||
QY 502 CTTCACCTTGGCTGAAAGGCGCCAGGACGACTTCCACATGATCTGAGACTTCCAGC 561
    |||
    |||
    |||
Db 387 CTTCACCTTGGCTGAAAGGCGCCAGGACGACTTCCACATGATCTGAGACTTCCAGC 446
    |||
    |||
    |||
QY 562 AGCCTAATGAGTCTGTGCTTATTTGTGACAGCTTTGGAAAAGACAGGCACTAAGTCTGTG 621
    |||
    |||
    |||
Db 447 AGCCTAATGAGTCTGTGCTTATTTGTGACAGCTTTGGAAAAGACAGGCACTAAGTCTGTG 506
    |||
    |||
    |||
QY 622 CAGACTTAAACGCGCAGAGACTTCTGTTTCTATCAAGGCTCTTTCGATACACAGAAAC 681
    |||
    |||
    |||
Db 507 CAGACTTAAACGCGCAGAGACTTCTGTTTCTATCAAGGCTCTTTCGATACACAGAAAC 566
    |||
    |||
    |||
QY 682 TCGCCATGCGATGAGGGAAGTTCTGTGAGGGCTCCATCGCATCTGAAAGCTTGCAC 741
    |||
    |||
    |||
Db 567 TCTCTA-----GTGCGCTTTTCAACCTGCGCAAGCTTGTCA 602
    |||
    |||
    |||
QY 742 AGTCGAAATGTCCTCCGCGGACAGTGTGACTTCCGTGCTCACTGTGCGGACAC 801
    |||
    |||
    |||
Db 603 GGCATGATACGAAACGAAAGGCGAGATTACTTCTTAAGGCCACTTCTTCAACCTTCA 662
    |||
    |||
    |||
QY 802 AGCAGAGATTCAGAGGGCGGACACTAAGTGG--AAGCCTTACACTCAATGAGAGCG 859
    |||
    |||
    |||
Db 663 TGGAACTCGGAGAGCTGCCCCAAGGCACTGCGCATCCACGTACTGTACAAGATTC 722
    |||
    |||
    |||
QY 860 ACTTAATGCAAACTCTACTGTATTCGCAAGAGATTTGATTTCTTTTCTTTTGTCAATA 919
    |||
    |||
    |||
Db 723 ACAGAGCCCAATGCTCTGCGGGCCAGTGAAGTCTCGTGAACCTC-----AAG 770
    |||
    |||
    |||
QY 920 AAGTCAAAAGATGGCACTTCATGCTCGAGAGATAGCCGTAATGTTTATATGATGAGAT 979
    |||
    |||
    |||
Db 771 ACATGGAGCTGTGCACATCAACCCCTGCACAGAGCGACTTCCGCTGAGACTGCACAA 830
    |||
    |||
    |||
QY 980 GTGAGCTAGTGTGTGTCACATCTGC--GCACATGCCCCAGCCCTCCAGGAAAGACCTC 1038
    |||
    |||
    |||
Db 831 AAGCAGCATTTCTGTGGAAGAGCGCAAGAAATACATGCCAGCTCCCAAGGAAAGACCTC 890
    |||
    |||
    |||
QY 1039 TTCACTTCCAGATGATGATATAGTCTTCTTACGGCAATTAAGCGCTCTTCTGAGTCC 1098
    |||
    |||
    |||
Db 891 TTCACTTCCAGATGATGATATAGTCTTCTTACGGCAATTAAGCGCTCTTCTGAGTCC 950
    |||
    |||
    |||
QY 1099 CATGAATATGAAGACTGAACGTGAGACCTTGGTGTGTGTGACAAAAGATGACAA 1158
    |||
    |||
    |||
Db 951 CATGAATATGAAGACTGAACGTGAGACCTTGGTGTGTGTGACAAAAGATGACAA 1010
    |||
    |||
    |||
QY 1159 AACCATGGCATGAAAATATACCAACCTAAGTGTGATGATGATCAATGATGATCTCT 1218
    |||
    |||
    |||
Db 1011 AACCATGGCATGAAAATATACCAACCTAAGTGTGATGATGATCAATGATGATCTCT 1070
    |||
    |||
    |||
QY 1219 TTATTTCAAGA----- 1229
    |||
    |||
    |||
Db 1071 TTATTTCAAGAATGGAACAATAGAGAAACATCAATTCGATTTAGTGTGATTTCTT 1130
    |||
    |||
    |||
QY 1230 ----- 1229
    |||
    |||
    |||
Db 1131 CTAGAAATGAACAGCCAGACTGTGTATTAATGACACAGCAGACACACCTTAATGATGC 1190
    |||
    |||
    |||
QY 1230 -----TGATTAATGAGGGAAGTGGGACTGTCATGACACAGGCTATC 1272
    |||
    |||
    |||
```

Db 1191 TTCTCCAGATGGCAGTCTGGATTGATGGGGAAAGATGGGACCTGCTATGACCAAGCCATTC 1250  
QY 1273 TTACTGACTGGTCTGGATTATATGTCTCTGGAGAAATGAGCCCTGTGACACTTTGGGATTT 1332  
Db 1251 TTAATGACTGGTCTGGATTATATGTCTCTGGAGAAATGAGCCCTGTGACACTTTGGGATTT 1310  
QY 1333 GCACCCATAAGTGGAAATGTGTAGTAAATATCGACGTGACAGATTATAGAAATACAGGT 1392  
Db 1311 GCACCCATAGTGGAAATGTGTAGTAAATATCGACGTGACAGATTATAGAAATACAGGT 1370  
QY 1393 CTTGGACTGGCTTCAACCATTTGCCATGAGTCTGACACAACTTTGGCATGATTCATGAT 1452  
Db 1371 CTTGGACTGGCTTCAACCATTTGCCATGAGTCTGACACAACTTTGGCATGATTCATGAT 1430  
QY 1453 GGAAGAGGGAACATGTGTAAAGTCCGAGGGGCAATCATGCTCCCTCATTTGGAGAGA 1512  
Db 1431 GGAAGAGGGAACATGTGTAAAGTCCGAGGGGCAATCATGCTCCCTCATTTGGAGAGA 1490  
QY 1513 CGCAATGAGAGTCTTCTCTCTGGTCAACCCCTGACGCCGCAATCTACACAAATTTCTTAAG 1572  
Db 1491 CGCAATGAGAGTCTTCTCTCTGGTCAACCCCTGACGCCGCAATCTACACAAATTTCTTAAG 1550  
QY 1573 ACCGCTCAAGCTATCTGCTCTGCTGATCAGCCCAAGCTGTGAAGAAATCAAGTATCCT 1632  
Db 1551 ACCGCTCAAGCTATCTGCTCTGCTGATCAGCCCAAGCTGTGAAGAAATCAAGTATCCT 1610  
QY 1633 GGAATATGCGACGAGAAATTTATATGATGCAACACACAGTGCAGTGGGAGTTCCGAGAG 1692  
Db 1611 GGAATATGCGACGAGAAATTTATATGATGCAACACACAGTGCAGTGGGAGTTCCGAGAG 1670  
QY 1693 AAAGCAAGCTCTGCATGCTGGAATTAAAGAGACATCTGTAAAGCCCTGTGTGCCAT 1752  
Db 1671 AAAGCAAGCTCTGCATGCTGGAATTAAAGAGACATCTGTAAAGCCCTGTGTGCCAT 1730  
QY 1753 CGTATTGGAAGAAATGTGAGACTAAATTTATGCCAGACAGAGACACAAATTTGTGGG 1812  
Db 1731 CGTATTGGAAGAAATGTGAGACTAAATTTATGCCAGACAGAGACACAAATTTGTGGG 1790  
QY 1813 CATGACATGTGTGCGGGGAGGACAGTGTGTAAATATGTGTGAAGGCCCCAAGCCC 1872  
Db 1791 CATGACATGTGTGCGGGGAGGACAGTGTGTAAATATGTGTGAAGGCCCCAAGCCC 1850  
QY 1873 ACCCATGCGCACTGTGCGAGCTGTGCTTCTTGGTCCCAATGCTCCAGACCTGCGAGGG 1932  
Db 1851 ACCCATGCGCACTGTGCGAGCTGTGCTTCTTGGTCCCAATGCTCCAGACCTGCGAGGG 1910  
QY 1933 GGAATATCTCATAGAGTGGCTCTGTCACCAACCCCAAGCCATGCGATGGAAGGAAGTTC 1992  
Db 1911 GGAATATCTCATAGAGTGGCTCTGTCACCAACCCCAAGCCATGCGATGGAAGGAAGTTC 1970  
QY 1993 TGTGAAGGCTCCCATGCGACTCTGGAAGCTCTGCAACAGTCAAGAAATGTCCCCGGGACAGT 2052  
Db 1971 TGTGAAGGCTCCCATGCGACTCTGGAAGCTCTGCAACAGTCAAGAAATGTCCCCGGGACAGT 2030  
QY 2053 GTTGAATCCGTCCTGCTCAGTGTGCGAGCAACAGCAGAGATTCAGAGGGCGGAC 2112  
Db 2031 GTTGAATCCGTCCTGCTCAGTGTGCGAGCAACAGCAGAGATTCAGAGGGCGGAC 2090  
QY 2113 TACAGTGAAGCTTACCTACCTACAGTGAAGATCAGACTTATGCAAACTTACTGTATC 2172  
Db 2091 TACAGTGAAGCTTACCTACCTACAGTGAAGATCAGACTTATGCAAACTTACTGTATC 2150  
QY 2173 GCGAAGAGATTTGATTTCTTTCTTTGTCAAAATTAAGTCAAAATGGAAGTCCATG 2232  
Db 2151 GCGAAGAGATTTGATTTCTTTCTTTGTCAAAATTAAGTCAAAATGGAAGTCCATG 2210  
QY 2233 TCGAGAGATGACCGTATGTTGTATAGATGGGATATGTGAGAGAGTTGGATGCAAT 2292  
Db 2211 TCGAGAGATGACCGTATGTTGTATAGATGGGATATGTGAGAGAGTTGGATGCAAT 2270  
QY 2293 GTCTCTGATCTGATGCTGTGAAGAGCTGTGTGGGGTGTGTAACGGAAATTAATCAACC 2352  
Db 2271 GTCTCTGATCTGATGCTGTGTGAAGAGCTGTGTGGGGTGTGTAACGGAAATTAATCAACC 2330

QY 2353 TGCAGATTCACAGGGGCTCTACACCAAGACCAACCAACCAAGTATTATCACATG 2412  
Db 2331 TGCAGATTCACAGGGGCTCTACACCAAGACCAACCAACCAAGTATTATCACATG 2390  
QY 2413 GTACCAATTCCTTCTGAGACCCCGAGATATCCGATCTATGAATGAACGTCTCTACCTCC 2472  
Db 2391 GTACCAATTCCTTCTGAGACCCCGAGATATCCGATCTATGAATGAACGTCTCTACCTCC 2450  
QY 2473 TACATTTCTGTGCGCAATGCCCTCAGAAAGTACTACCTGAATGGGACCTGGAC 2532  
Db 2451 TACATTTCTGTGCGCAATGCCCTCAGAAAGTACTACCTGAATGGGACCTGGAC 2510  
QY 2533 TGGCCCGGCGGTACAAATTTTCGGGCACTATTTCGATACAGACGCTCTATATGAG 2592  
Db 2511 TGGCCCGGCGGTACAAATTTTCGGGCACTATTTCGATACAGACGCTCTATATGAG 2570  
QY 2593 CCGAGAACTTATATGCTATCTGACCAACCAACGAGACATGATTTGGAGCTGCTGTTT 2652  
Db 2571 CCGAGAACTTATATGCTATCTGACCAACCAACGAGACATGATTTGGAGCTGCTGTTT 2630  
QY 2653 CAGGAGGAACCCGGGTGTGCTGCGGAATATCTCAATGCTGCTTGGGGACCGGAGAG 2712  
Db 2631 CAGGAGGAACCCGGGTGTGCTGCGGAATATCTCAATGCTGCTTGGGGACCGGAGAG 2690  
QY 2713 CAGCCCTGCGCCAGGCCAGCTTACATTTGGGCAATGTCGCTGAGTGTCCGCTGTC 2772  
Db 2691 CAGCCCTGCGCCAGGCCAGCTTACATTTGGGCAATGTCGCTGAGTGTCCGCTGTC 2750  
QY 2773 TCGGAGGGGG 2783  
Db 2751 TCGGAGGGGG 2761

RESULT 10  
US-09-981-151A-3  
; Sequence 3, Application US/0981151A  
; Publication No. US20030212256A1  
; GENERAL INFORMATION:  
; APPLICANT: Edinger, Shlomit R  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: MacDougall, John R  
; APPLICANT: Malysankar, Muriel M  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Reymen, John A  
; APPLICANT: Stone, David J  
; APPLICANT: Gunther, Erik  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Shinkels, Richard A  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Patlurajan, Meera  
; APPLICANT: Taupier Jr, Raymond J  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Zerhusen, Bryan D  
; APPLICANT: Kerkula, Ramesh  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Gangolli, Esna A  
; APPLICANT: Fernandes, Elma R  
; APPLICANT: Gorman, Linda  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-168  
; CURRENT APPLICATION NUMBER: US/09/981,151A  
; PRIOR FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 60/241,040  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/241,058  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/241,063  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/241,243  
; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/242,152
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/242,482
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/242,611
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/242,612
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/242,880
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: 60/242,881
 ; PRIOR FILING DATE: 2000-10-24
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 160
 ; SOFTWARE: Patent Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 2433
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-981-151A-3

Query Match 62.0%; Score 1795.6; DB 10; Length 2433;
 Best Local Similarity 82.0%; Pred. No. 0;
 Matches 2375; Conservative 0; Mismatches 34; Indels 489; Gaps 7;

QY 1 CGCTCTGATGAAGCCCGCGCGCGGATGCGGGGCTTGCGGCGCTGTGATGCTG 60
 DB 22 CGTCTCTGATGAAGCCCGCGCGCGGATGCGGGGCTTGCGGCGCTGTGATGCTG 81
 QY 61 TTGGGCGAGTGGCGGAGGATGATCCCGGGCGCTCCACAGGCGGAAACCGCGGG 120
 DB 82 CTGGCCAGATGGCCGAGCGATGATCCCGGGCGCTCCACAGGCGGAAACCGCGGG 141
 QY 121 TCCGGAAGCTGAGGCGAGTCCCGCGCGCTCTCTCCGCGGACCCCGCGCTCACC 180
 DB 142 TCCGGAAGCTGAGGCGAGTCCCGCGCGCTCTCTCCGCGGACCCCGCGCTCACC 201
 QY 181 GGGATGTCCCGCTGTTTTCGCGAGGACCTGCTGCGCATGAGACCCGCGAGCAGC 240
 DB 202 GGGATGTCCCGCTGTTTTCGCGAGGACCTGCTGCGCATGAGACCCGCGAGCAGC 261
 QY 241 GCGTGGAGACCCGAGCGTCCCGGCTCTCTCCACCCGCGGAGCGGGCTGATGGA 300
 DB 262 GCGTGGAGACCCGAGCGTCCCGGCTCTCTCCACCCGCGGAGCGGGCTGATGGA 321
 QY 301 AAAGGCGGAGCATGATGATGAGTGAACATCGTTCTCAGCAACTAAACAGGACA 360
 DB 322 AAAGGCGGAGCATGATGATGAGTGAACATCGTTCTCAGCAACTAAACAGGACA 381
 QY 361 GAAACCAAACTGATGATGTTCTCACTC--AATATGACCTGCTCTGCTTACGAGTT 417
 DB 382 GAAACCAAACTGATGATGTTCTCACTC--AATATGACCTGCTCTGCTTACGAGTT 441
 QY 418 GACACAGGGGCGATTAAGTGTCCCATGAATCATATGACATCAGGCGGAGGAGAGA 477
 DB 442 GACACAGGGGCGATTAAGTGTCCCATGAATCATATGACATCAGGCGGAGGAGAGA 501
 QY 478 GTGGCCGCTGTCCGAGGTTAGTCTCTTCACTTCGCTGTAAGGCGCCGAGGACGATTC 537
 DB 502 GTGGCCGCTGTCCGAGGTTAGTCTCTTCACTTCGCTGTAAGGCGCCGAGGACGATTC 561
 QY 538 CACATGATCTGAGGCTTCGAGGAGCTTATGAGGCTCTGCGCTTATTTGTGACAGTTG 597
 DB 562 CACATGATCTGAGGCTTCGAGGAGCTTATGAGGCTCTGCGCTTATTTGTGACAGTTG 621
 QY 598 GGAAGAAGAGGAGCTTAAGTGTGAGGATTTACCGCGAGAGAGAGCTTCTGTTATCA 657
 DB 622 GGAAGAAGAGGAGCTTAAGTGTGAGGATTTACCGCGAGAGAGAGCTTCTGTTATCA 681
 QY 658 GGCCTTTTGCATCAACAGAACTGCGCATGCGATGAGGAGAGTTCTGTGAGGCTCC 717
 DB 682 GGCCTTTTGCATCAACAGAACTGCGCATGCGATGAGGAGAGTTCTGTGAGGCTCC 741

QY 718 ACTGCACTCTGAGACCTCTGCAACAGTCAGAAATGTCCCGGAGACGTGTGACTTCGCT 777
 DB 742 ACTGCACTCTGAGACCTCTGCAACAGTCAGAAATGTCCCGGAGACGTGTGACTTCGCT 801
 QY 778 GGTGCTCAGTGTGCGGAGCAACAGCAGATTCAGAGGGCGGACCTACAGTGGAAAG 837
 DB 802 GGTGCTCAGTGTGCGGAGCAACAGCAGATTCAGAGGGCGGACCTACAGTGGAAAG 861
 QY 838 CCTTACACTCAAGTGAAGCCGACTTATGCAAACTCTACTGTATGCGAAGAGATTGAT 897
 DB 862 CCTTACACTCAAGTGAAGCCGACTTATGCAAACTCTACTGTATGCGAAGAGATTGAT 921
 QY 898 TTCTCTTTTCTTTTGTCAATTAAGTCAAATGAGTGGAGCTCCATGCTCGAGAGATGCGCT 957
 DB 922 TTCTCTTTTCTTTTGTCAATTAAGTCAAATGAGTGGAGCTCCATGCTCGAGAGATGCGCT 981
 QY 958 AATGTTGATTAAGTGAAGATTAAGTGAAGTCAAGTGTGTCACATCTGCGGACATGCGCC 1017
 DB 982 AATGTTGATTAAGTGAAGATTAAGTGAAGTCAAGTGTGTCACATCTGCGGACATGCGCC 1014
 QY 1018 CAGCTCCCAAGAGAGACCTCTTCACTTGTGCGAGTGAATTAAGTCTTACGCGCAT 1077
 DB 1015 CAGCTCCCAAGAGAGACCTCTTCACTTGTGCGAGTGAATTAAGTCTTACGCGCAT 1074
 QY 1078 AAGCCTCTCTTCTGAGGTCCCATGAAATGAAGACTGAACGTGAGACCTTGTGCTG 1137
 DB 1075 AAGCCTCTCTTCTGAGGTCCCATGAAATGAAGACTGAAGCTGAGACCTTGTGCTG 1134
 QY 1138 GTGCAAAAGAGATGATGCAAAACCATGAGCCATGAAATATCAGCAGCTGATGCTCAG 1197
 DB 1135 GTGCAAAAGAGATGATGCAAAACCATGAGCCATGAAATATCAGCAGCTGATGCTCAG 1194
 QY 1198 ATACTCAACATGATATCTGCTTATTCAAAGATGATGAGGAAAGATGAGGACTCGT 1257
 DB 1195 ATACTCAACATGATATCTGCTTATTCAAAGATGATGAGGAAAGATGAGGACTCGT 1238
 QY 1258 CATGACACGCGATCTTACTGACTGTGCTGATATATGTTCTGTGAAGATGAGCCCTGT 1317
 DB 1239 ----- 1238
 QY 1318 GACACTTTGGGATTTGACCCATTAAGTGAATGATGAATATTCGAGCTGACGATTT 1377
 DB 1239 -----AGGAACATCAACATTGCAATTGT 1262
 QY 1378 AATGAAGATACAGGCTTGAACCTGCGCTTCAACATTGCGCATGAGCTGGAACAATTT 1437
 DB 1263 AGGCTGATTC----- 1273
 QY 1438 GGCATGATTCATGATGAGGAAGGAACATGTGTAAAAAGTCCGAGGCAACATCATGTCC 1497
 DB 1274 ----- 1273
 QY 1498 CTTACATTGGAGAGACGCAATGAGATCTTCTCTGTGTCAACCTGACCGCCAGATCTTA 1557
 DB 1274 ----- 1273
 QY 1558 CACAATTTCTAAGCACGCTCAAGCTATCTGCTGTGATCAGCCAAAGCTGTGAAG 1617
 DB 1274 ----- 1273
 QY 1618 GAATTAAGTATCTGAGAAATTTGCCAGAGAAATTAATGATGCAAAACACAGTGCAG 1677
 DB 1274 ----- 1273
 QY 1678 TGGCAGTTCCGAGAGAAAGCAAGCTCTGACGTGACCTTTAAAGAGACATCTGTAA 1737
 DB 1274 -----TTCTTAAGATGAACAGAGACATCTGTAA 1302
 QY 1738 GCGCTGTGTGCATCGTATTTGGAAGAAATGTGAGACTTAATTTATTCGACAGCAGAA 1797
 DB 1303 GCGCTGTGTGCATCGTATTTGGAAGAAATGTGAGACTTAATTTATTCGACAGCAGAA 1362
 QY 1798 GGCACAAATTTGTGGCATGACATGTGTGCGGGAGAGACAGTGTGTGAAATATGTGAT 1857

1363 GGCAATTTGGGATGACATGTGTGCGGGAGAGACATGTGTGAATATGTGAT 1422  
1858 GAAGGCCCCAAGCCCACTGGGCACTGGTGGGACTGGCTTCTTGGTCCCATGCTCC 1917  
1423 GAAGGCCCCAAGCCCACTGGGCACTGGTGGGACTGGCTTCTTGGTCCCATGCTCC 1482  
1918 AGGACCTGGGAGGGGAGTATCTCATAGAGTGGCTCTGACCAACCCCAAGCCATCG 1977  
1483 AGGACCTGGGAGGGGAGTATCTCATAGAGTGGCTCTGACCAACCCCAAGCCATCG 1542  
1978 CATGAGGGAAGTTCTGTGAGGGCTCAGCTCGACTGTGAAGCTCTGCAACAGTCAGAA 2037  
1543 CATGAGGGAAGTTCTGTGAGGGCTCAGCTCGACTGTGAAGCTCTGCAACAGTCAGAA 1602  
2038 TGTCCCCGGGAGAGTGTGACTTCCGTCGCTCAGTGGCCGAGAGCAACAGCAGACGA 2097  
1603 TGTCCCCGGGAGAGTGTGACTTCCGTCGCTCAGTGGCCGAGAGCAACAGCAGACGA 1662  
2098 TTCAGAGGGCGGAGCTTACAGAGTGAAGCTTACACTCAAGTAGAAGTACAGACTTATGC 2157  
1663 TTCAGAGGGCGGAGCTTACAGAGTGAAGCTTACACTCAAGTAGAAGTACAGACTTATGC 1704  
2158 AAACTCTACTGATCCGAGAAAGATTTGATTTCTTTTCTTTGTCAATAAATGCAAA 2217  
1705 AAACTCTACTGATCCGAGAAAGATTTGATTTCTTTTCTTTGTCAATAAATGCAAA 1764  
2218 GATGGGATCCCACTGCTCGAGAGTACCCCTAATGTTGTATAGATGGGAAATGTGAGA 2277  
1765 GATGGGATCCCACTGCTCGAGAGTACCCCTAATGTTGTATAGATGGGAAATGTGAG-- 1821  
2278 GTTGATGTGACATGATCTCTTGGATCTGATGCTGTGAAGACGCTGTGGGGGTGTAAAC 2337  
1822 ---GGATGTGACATGATCTCTTGGATCTGATGCTGTGAAGACGCTGTGGGGGTGTAAAC 1878  
2338 GGGAAATTAATCTCAGCTCGACAGATTCACAGGGGTCTCTTACCAAGACCAACACCAAC 2397  
1879 GGGAAATTAATCTCAGCTCGACAGATTCACAGGGGTCTCTTACCAAGACCAACACCAAC 1938  
2398 CAGTATTAATCAATGATGATCCATTCCTCTGAGAGCCCGGAGTATCCGGCATCTATGAAGT 2457  
1939 ---TATTAATCAATGATGATCCATTCCTCTGAGAGCCCGGAGTATCCGGCATCTATGAAGT 1995  
2458 AACGTCTTAATCTCAGCTCGACAGATTCACAGGGGTCTCTTACCAAGACCAACACCAAC 2517  
1996 AACGTCTTAATCTCAGCTCGACAGATTCACAGGGGTCTCTTACCAAGACCAACACCAAC 2055  
2518 CACTGAGACGCTGAGCTGGCCCGGACGAGTCAAAATTTTCGGGCACTACTTTGACATACAG 2577  
2056 CACTGAGACGCTGAGCTGGCCCGGACGAGTCAAAATTTTCGGGCACTACTTTGACATACAG 2115  
2578 CGGTCTTAATTAAGCCCGGAGACCTTAATGCTATGCTATGACCAACCAACGAGACATGAT 2637  
2116 CGGTCTTAATTAAGCCCGGAGACCTTAATGCTATGCTATGACCAACCAACGAGACATGAT 2175  
2638 GTGAGACTGCTGTTTCAAGGAAAGAAACCCGGGTGTTGCTCGGAAATTAATCTCATGCTCGC 2697  
2176 GTGAGACTGCTGTTTCAAGGAAAGAAACCCGGGTGTTGCTCGGAAATTAATCTCATGCTCGC 2235  
2698 TTGGGAGACGAGAGAGACGCCCTGCGCAGCCAGCTTACACTTGGGCAATGTCGCTCT 2757  
2236 TTGGGAGACGAGAGAGACGCCCTGCGCAGCCAGCTTACACTTGGGCAATGTCGCTCT 2295  
2758 GAGTGTCTCCGTGTCTGCGAGAGGGGAGTATGCTTCAATGCTGTCTCTGAGAGGACGA 2817  
2296 GAGTGTCTCCGTGTCTGCGAGAGGGGAGTATGCTTCAATGCTGTCTCTGAGAGGACGA 2355  
2818 TGTCAAGCTTCAAGCTGAGTCAATTCGATGCTGCTTCTTGAATCTTAATAGCAGCC 2877  
2356 TGTCAAGCTTCAAGCTGAGTCAATTCGATGCTGCTTCTTGAATCTTAATAGCAGCC 2415  
2878 CCGGGCTTCTCCCTGCCA 2895

Db 2416 CCGGGCTTCTCCCTGCCA 2433  
RESULT 11  
US-09-981-151A-5  
Sequence 5, Application US/09981151A  
Publication No. US20030212256A1  
GENERAL INFORMATION:  
APPLICANT: Edinger, Shlomit R  
APPLICANT: Gerlach, Valerie  
APPLICANT: Macdougall, John R  
APPLICANT: Malyanekar, Muriel M  
APPLICANT: Smithson, Glenda  
APPLICANT: Millet, Isabelle  
APPLICANT: Peyman, John A  
APPLICANT: Stone, David J  
APPLICANT: Gunther, Erik  
APPLICANT: Ellerman, Karen  
APPLICANT: Shinkets, Richard A  
APPLICANT: Padigar, Muralidhara  
APPLICANT: Guo, Xiaojia  
APPLICANT: Paturajan, Meera  
APPLICANT: Taupier Jr, Raymond J  
APPLICANT: Burgess, Catherine E  
APPLICANT: Zehusen, Bryan D  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Spytek, Kimberly A  
APPLICANT: Gangolli, Esba A  
APPLICANT: Fernandes, Blma R  
APPLICANT: Gorman, Linda  
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-168  
CURRENT APPLICATION NUMBER: US/09/981,151A  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 60/241,040  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,058  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,063  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,243  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/242,152  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/242,482  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,611  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,612  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,880  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/242,881  
PRIOR FILING DATE: 2000-10-24  
Remaining Prior Application data removed - See file wrapper or PAM.  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 2902  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-981-151A-5  
Query Match 58.5%; Score 1695; DB 10; Length 2902;  
Best Local Similarity 78.1%; Pred. No. 0;  
Matches 2333; Conservative 0; Mismatches 315; Indels 339; Gaps 11;  
40 TTGGCGGCGCTGTGATGCTGTTGGCGCAGTGGCGGACAGATGATCCCGGCGCTCC 99  
1 TTGGCGGCGCTGTGATGCTGCTGGCGCAGTGGCGGACAGATGATGATCCCGGCGCTCC 60  
100 CACCAAGCGGAGAAACCGCGGCTCCGAGACGCTGAGAGCGAGTCCCGCGGCTCTCTCC 159

Db 61 CACGACGCGGAAACCGCGGCTCGGACAGCTGGAAGCCAGTCCCCCGGCGCTCTCTCC 120  
Qy 160 CCGGACCCCGCGCTCTCACCGGATGTGCGCGCTGTTTTCCGACGAGCACTGCGCGC 219  
| | | | |  
Db 121 CCGGACCCCGCGCTCTCACCGGATGTGCGCGCTGTTTTCCGACGAGCACTGCGCGC 180  
Qy 220 CATGGACCCGCGCGGAGCGGCTTGGAGCCCGAGGCTCCGCGTCTCTCCACCCG 279  
| | | | |  
Db 181 CATGGACCCGCGCGGAGCGGCTTGGAGCCCGAGGCTCCGCGTCTCTCCACCCG 235  
Qy 280 GAGGCGCGCGGCTGGATGGAAAAAGGCGGAGCATGGATGAAAGCTGGAAACATCGTTCT 339  
| | | | |  
Db 236 ----- 235  
Qy 340 CAGCAAACTAACACAGAGAAACAGAAAAACAACATGCTGATGTTCTCATCTGAATGACCTG 399  
| | | | |  
Db 236 -----GACCTG 241  
Qy 400 GTCTCTGCTTACGAGGTTGACACAGGGGCGATTACGTGTCCTCATGAAATCATGACCAT 459  
| | | | |  
Db 242 GTCTCTGCTTACGAGGTTGACACAGGGGCGATTACGTGTCCTCATGAAATCATGACCAT 301  
Qy 460 CAGCGCGGAGAAAGACAGTGGCGGTGTCGAGGTTGAGTCTCTTCACTTGGCGTGA 519  
| | | | |  
Db 302 CAGCGCGGAGAAAGACAGTGGCGGTGTCGAGGTTGAGCAGCCCTTCTCAGGTAATG 361  
Qy 520 GCGCGGAGGACGACTTCCACATGATCTGAGGACTTCCAGCAGCCCTAGTGGCTCTGCG 579  
| | | | |  
Db 362 AAGGCGGAGAGCTCAGACT-----GTGTGTGAGGCGCTTTCATGTGTAATTTCTCAGC 416  
Qy 580 TTTATTTGTGCAACGTTGGGAAAGACAGGCACTAATCTGTGAGACTTTACCGCCAGAG 639  
| | | | |  
Db 417 CCGGGTTTTTGAACCTTTCCAAATGTCGCTCTCACAGGAGAAACAGACTGTTCCAA 476  
Qy 640 GACTTCTGTTTTCTAAGGCTCTTGGCATCAACAGAAACCTGCGATCGCATGGAGG 699  
| | | | |  
Db 477 GATTAATAACAATGCA-----TGCTTGGAGAAATCGGCGCTTGCTTCAACAGAAAG 529  
Qy 700 AAGTTCTGTGAGGCGCTCACTGCGACTGTGAAGCTGTGCAACAGTCAAAATGTCCCG 759  
| | | | |  
Db 530 TCTAATGTGTGTTTTCTTCTTCTTTTATTTTTCACGTCAAGGACATGATAGAACAG 589  
Qy 760 GACAGTGTGACTTCCGTGCTGTCACTGAGTGGCCGAGCAACAGCAGAGATTCAGAGG 819  
| | | | |  
Db 590 GAGGAGATTAATCTCTTGAAGCCACTTCTTCAACCTCTCAATGAGAACTCGGCGAGAG 649  
Qy 820 CCGACTTACAAGTG--AAGCTTACACTCAAGTAAAGCCGACTAATGCAAACTACT 877  
| | | | |  
Db 650 GCCCAAGGAGCTCGGCACTCCACGTACTGTACAGAGAGAGGTCTGTGACCTTCAAG 709  
Qy 878 GTATGCGAGAAAGATTTGATTTCTTCTTCTTGTCAATAAAGTCAAAAGTGGGACTC 937  
| | | | |  
Db 710 ACATGGAGAC-----TGGCATCAATCAACCCCTGCAAGAGCGA 747  
Qy 938 CATGCTCGAGAGATAGCCGTAATGTTTGTATAGATGGATATGTGAGCTCACTGTGCT 997  
| | | | |  
Db 748 CTTTGCGCTGGGACTGCGCAAAAGCAGATTTCTGTGAAAGCGCAGMAAAT----- 800  
Qy 998 CCACATCTGCGCATGCGCCAGCGCTCCGAGAGAAAGCTTTCACTTTGCGAGATGAGT 1057  
| | | | |  
Db 801 -----ACATGCCCCAGCTCCCAAGGAGAGCTTTCACTTTGCGAGATGAGT 848  
Qy 1058 ATTAAGTCTTGTCTTAACGCAATTAAGCGCTCTTCTGAGGTCCCATTAAGAAATGAAGACTGA 1117  
| | | | |  
Db 849 ATTAAGTCTTGTCTTAACGCAATTAAGCGCTCTTCTGAGGTCCCATTAAGAAATGAAGACTGA 908  
Qy 1118 AGTGGAGACCTTGTGTGTGTGTGCAAAAAAGATGATGCAAAAACTATGCGCCATGAATAA 1177  
| | | | |  
Db 909 AGTGGAGACCTTGTGTGTGTGTGCAAAAAAGATGATGCAAAAACTATGCGCCATGAATAA 968  
Qy 1178 TCACCACTACAGTGTCTCAAGATCTCAACATGTATCTGCTTTATTAATCAAGA----- 1229  
| | | | |  
Db 969 TCACCACTACAGTGTCTCAAGATCTCAACATGTATCTGCTTTATTAATCAAGAATGAACAA 1028

Qy 1230 ----- 1229  
Db 1029 TAGAGAAACATCAACATTTGCATTTGATAGTCTGATTTCTTATAGAAATGAACAGCCAG 1088  
Qy 1230 -----TG 1231  
Db 1089 GACTGTGATTAATGTCACACGAGCAACAACCTTAAGTATTTCTGCAAGTGGAGTCTG 1148  
Qy 1232 GATTATGGGAGAAAGATGGAGACTCGTCAATGACACAGCCATCTTACATGCTGTGATA 1291  
| | | | |  
Db 1149 GATTATGGGAGAAAGATGGAGCTCGTCAATGACACGCCATCTTACTGACTGTGTGATA 1208  
Qy 1292 TATGTTCTGGAAGATGAGCCCTGTGACACTTTGGGATTTGCAACCCATTAAGTGAATGT 1351  
| | | | |  
Db 1209 TATGTTCTGGAAGATGAGCCCTGTGACACTTTGGGATTTGCAACCCATTAAGTGAATGT 1268  
Qy 1352 GTAGTAAATATTCGACGCTGACAGATTAATGAAGATACAGGCTTTGGACTGGCTTCAACA 1411  
| | | | |  
Db 1269 GTAGTAAATATTCGACGCTGACAGATTAATGAAGATACAGGCTTTGGACTGGCTTCAACA 1328  
Qy 1412 TTGCCATGAGTCTGAGACAACTTTGGCATGATTCATGATGAGAGAGAAACATGTGTA 1471  
| | | | |  
Db 1329 TTGCCATGAGTCTGAGACAACTTTGGCATGATTCATGATGAGAGAGAAACATGTGTA 1388  
Qy 1472 AAAAGTCCGAGGGAACATCATGTCCTCCCTACATTTGGCAGAGAGCAATGAGTCTTCTCT 1531  
| | | | |  
Db 1389 AAAAGTCCGAGGGAACATCATGTCCTCCCTACATTTGGCAGAGAGCAATGAGTCTTCTCT 1448  
Qy 1532 GGTCAACCTGACCGCGGCAATCTACAAATTTCTAAGCACCGCTCAAGCTATCTGCG 1591  
| | | | |  
Db 1449 GGTCAACCTGACCGCGGCAATCTACAAATTTCTAAGCACCGCTCAAGCTATCTGCG 1508  
Qy 1592 TTGCTGATCAGCCAAAGCTGTGAAGAAATCAAGTATCTGAGAAATTTGCCAGAGAAAT 1651  
| | | | |  
Db 1509 TTGCTGATCAGCCAAAGCTGTGAAGAAATCAAGTATCTGAGAAATTTGCCAGAGAAAT 1568  
Qy 1652 TATATGATGCAAAACACAGTGCAGAGTGGCAGTTGGAGAGAAACCAAGCTCTGCATGC 1711  
| | | | |  
Db 1569 TATATGATGCAAAACACAGTGCAGAGTGGCAGTTGGAGAGAAACCAAGCTCTGCATGC 1628  
Qy 1712 TGGACTTTTAAAGACATCTGTAAAGCCCTGTGTGCTATCTGTATTTGAAAGAAATGTG 1771  
| | | | |  
Db 1629 TGGACTTTTAAAGACATCTGTAAAGCCCTGTGTGCTATCTGTATTTGAAAGAAATGTG 1688  
Qy 1772 AGACTAAATTTATGCGACAGACAGAGGACAAATTTGTGGCATGACATGTGTCCCGG 1831  
| | | | |  
Db 1689 AGACTAAATTTATGCGACAGACAGAGGACAAATTTGTGGCATGACATGTGTCC--G 1745  
Qy 1832 GAGGACAGTGTGAAATATGTGTGTAAGGCCCCAGCCCAAGCCCATGAGGCACTGATGCG 1891  
| | | | |  
Db 1746 GAGGACAGTGTGAAATATGTGTGTAAGGCCCCAGCCCAAGCCCATGAGGCACTGATGCG 1805  
Qy 1892 ACTGTCTTTTGTGCCCCCATGCTTCACAGACCTGTGGAGGGGGAGTATCTCATAGAGTGC 1951  
| | | | |  
Db 1806 ACTGTCTTTTGTGCCCCCATGCTTCACAGACCTGTGGAGGGGGAGTATCTCATAGAGTGC 1865  
Qy 1952 GC-----CTGTGACCAACCCCAAGCCATGCGATGAGGAGAAATTTCTGTAGGAGCTCACTC 2008  
| | | | |  
Db 1866 GCTCTCAAAATACACTTCCAGGCGCATGCAATGAGGAGAAATTTCTGTAGGAGCTCACTC 1925  
Qy 2009 GCACTCTGAAGCTGTGCAACAGTCAAGAAATGTCCCCGGGACAGTGTGACTTCCGTGCTG 2068  
| | | | |  
Db 1926 GCACTCTGAAGCTGTGCAACAGTCAAGAAATGTCCCCGGGACAGTGTGACTTCCGTGCTG 1985  
Qy 2069 CTCAGTGTGCGAGAGACAAACAGAGACGATTCAGAGGCGGCACTACAAAGTGGAGCCCTT 2128  
| | | | |  
Db 1986 CTCAGTGTGCGAGAGACAAACAGAGACGATTCAGAGGCGGCACTACAAAGTGGAGCCCT- 2044  
Qy 2129 ACACCTCAAGTGAAGATCAGAGCTTATGCAAACTCTACTGTATGCGACAGAGAAATTTGATT 2188  
| | | | |  
Db 2045 -----GATAGAGACTTATGCAAACTCTACTGTATGCGACAGAGAAATTTGATT 2090



Qy	2189	TCTTCTTTCTTTGCAATTAAGCAAAATGGAATCGCANTGCTCGGAGATAGCGGTA	2248
Db	2091	TCTTCTTTCTTTGCAATTAAGCAAAATGGAATCGCANTGCTCGGAGATAGCGGTA	2150
Qy	2249	ATGTTTGTATGATGGGATATGTGAGAGATTGATGTGACATATGCTCTTGATCTGATG	2308
Db	2151	ATGTTTGTATGATGGGATATGTGAGAGATTGATGTGACATATGCTCTTGATCTGATG	2210
Qy	2309	CTGTTGAAGACGTCTGTGGGGTGTGTAAACGGGAATTACTAGCCTGACGATTCACAGG	2368
Db	2211	CTGTTGAAGACGTCTGTGGGGTGTGTAAACGGGAATTACTAGCCTGACGATTCACAGG	2270
Qy	2369	GTCCTCTAACCAAGACCAACCAACCAACCACTATATCAATATGTCCATTCCTCTG	2428
Db	2271	GTCCTCTAACCAAGACCAACCAACCAACCACTATATCAATATGTCCATTCCTCTG	2312
Qy	2429	GAGCCCGGAGATCCGCATCTATGAATAAGAACGTCTTACCTCCATCTTCTGAGCA	2488
Db	2313	GAGCCCGGAGATCCGCATCTATGAATAAGAACGTCTTACCTCCATCTTCTGAGCA	2372
Qy	2489	ATGCCCTCAGAAAGTACTACCTGAATGGGCACTGGAACGTGGAATGGCCCGGTA	2548
Db	2373	ATGCCCTCAGAAAGTACTACCTGAATGGGCACTGGAACGTGGAATGGCCCGGTA	2432
Qy	2549	AATTTTGGGGCACTTCTTGCATCAACGCTCCTATTAATAGCCCGGCAATTAATG	2608
Db	2433	AATTTTGGGGCACTTCTTGCATCAACGCTCCTATTAATAGCCCGGCAATTAATG	2492
Qy	2609	CTACTGACCAACCAACGAGACCTGATTTGTGAGCTCTGTTCAGGGGAAGAACCCG	2668
Db	2493	CTACTGACCAACCAACGAGACCTGATTTGTGAGCTCTGTTCAGGGGAAGAACCCG	2552
Qy	2669	GTGTTGCCCTGGGAATATCTCAATGCCCTGTGGGACCGAAGAGAGCCCTGCGCAGC	2728
Db	2553	GTGTTGCCCTGGGAATATCTCAATGCCCTGTGGGACCGAAGAGAGCCCTGCGCAGC	2612
Qy	2729	CCAGCTACACTTTGGGCACTGCTGCGCTCTGAGTCTCCGTCTCTGCGGAGGGGTAGT	2788
Db	2613	CCAGCTACACTTTGGGCACTGCTGCGCTCTGAGTCTCCGTCTCTGCGGAGGGGTAGT	2672
Qy	2789	GCCTTCCAGTGTGCTCCTGGAAGGAGAGATGACGCTTCAGGCACTGCGTACATTTGAC	2848
Db	2673	GCCTTCCAGTGTGCTCCTGGAAGGAGAGATGACGCTTCAGGCACTGCGTACATTTGAC	2732
Qy	2849	TGGCCTTCTTGAATCCTAATAGCAGCCCGGGCTTCTCCCTGCA	2895
Db	2733	TGGCCTTCTTGAATCCTAATAGCAGCCCGGGCTTCTCCCTGCA	2779
RESULT 12			
US-10-399-645-19			
; Sequence 19, Application US/10399645			
; Publication No. US20040029249A1			
GENERAL INFORMATION:			
; APPLICANT: INCYTE CORPORATION; LEB, Ernestine A.			
; APPLICANT: HAFALIA, April J.A.; YUE, Henry			
; APPLICANT: LAL, Preeti G.; YAO, Monique G.			
; APPLICANT: LU, Yan; CHAWLA, Nandinder K.			
; APPLICANT: WARREN, Bridget A.; LU, Dying Aina M.			
; APPLICANT: BAUGHN, Marian R.; DELBESANE, Angelo M.			
; APPLICANT: BURFORD, Neil; BOROWSKI, Mark L.			
; APPLICANT: LEB, Sally; XU, Yuming			
; APPLICANT: GRIEFIN, Jennifer A.; KULLICK, Deborah A.			
; APPLICANT: GANDHI, Ameena R.; ARVIZU, Chandra S.			
; APPLICANT: ISON, Craig H.; TANG, Y. Tom			
; APPLICANT: AZIMZAI, Yalda; ELLIOTT, Vicki S.			
; APPLICANT: SWARNANAR, Anita; RAMKUDAR, Jayalaxmi			
; APPLICANT: NGUYEN, Daniel B.; TRIBOULEY, Catherine M.			
; APPLICANT: LO, Terence P.; AU-YOUNG, Janice K.			
; APPLICANT: THANGAVELU, Kavilcha; KEARNEY, Liam			
TITLE OF INVENTION: PROTEASES			
FILE REFERENCE: PI-0263 USN			
; CURRENT APPLICATION NUMBER: US/10/399, 645			

	Query Match	56.6%; Score 1638; DB 17; Length 4888;	
Query	1010 ACATGCCCCAGCCTCCCAAGAGAACCTCTTCATCTTTCAGATGATGATATAGTCTTGGCT	Best Local Similarity 93.4%; Pred. No. 0;	
Db	803 ACATGCCCCAGCCTCCCAAGAGAACCTCTTCATCTTTCAGATGATGATATAGTCTTGGCT	Matches 1774; Conservative 0; Mismatches 0; Indels 126; Gaps 1;	
Query	1070 TACGGCATAAGCGCTCTCTTCTGAGGTCCTCAATGAAATGAAAGAACTGAGTGAAGACT		
Db	863 TACGGCATAAGCGCTCTCTTCTGAGGTCCTCAATGAAATGAAAGAACTGAGTGAAGACT		
Query	1130 TGGGTGGGTGTCGACAAAGAGATGATGCAAAACCATGGCCATGAAATATACACCACTTACG		
Db	923 TGGGTGGGTGTCGACAAAGAGATGATGCAAAACCATGGCCATGAAATATACACCACTTACG		
Query	1190 TGCTCAGATATCTCAACATGGTATCTGCTTATTTCAAAGA-----		
Db	983 TGCTCAGATATCTCAACATGGTATCTGCTTATTTCAAAGATGAAACAATAGAGAGAAACA		
Query	1230 -----		
Db	1043 TCAACATTGCAATTGTAGTCTGTATCTCTAGAAAGATGAAACGACGACGACTGGTATTA		
Query	1230 -----TGAGTATGAGGGGA		
Db	1103 GTCAACACGACACCAACCTTAAATGATCTTGCACATGGCACTGTGAGTATGATGAGGGA		
Query	1244 AAGATGGGACTGCTGATGACCAACGCACTTTTACCTGACTGGTATGATATATGTTCTTGA		
Db	1163 AAGATGGGACTGCTGATGACCAACGCACTTTTACCTGACTGGTATGATATATGTTCTTGA		
Query	1304 AGAATGAGCCCTGTGACACTTGGGATTTTGCAACCCATTAAGTGAATGTGATGAAATATTC		
Db	1223 AGAATGAGCCCTGTGACACTTGGGATTTTGCAACCCATTAAGTGAATGTGATGAAATATTC		
Query	1364 GCAAGTGGCAAGATTAATGAAGATPACAAGTCTTGGACATGGCTTCAACCATTTGCCCATAGT		
Db	1283 GCAAGTGGCAAGATTAATGAAGATPACAAGTCTTGGACATGGCTTCAACCATTTGCCCATAGT		
Query	1424 CTGGAACAACAATTGGCATATTCATATGATGAGAAAGGAAACATGTGTAAAAAGTCCGAGG		
Db	1343 CTGGAACAACAATTGGCATATTCATATGATGAGAAAGGAAACATGTGTAAAAAGTCCGAGG		
Query	1484 GCAACATCATATGTCCTTACATTGGCAGACGCAATGAGATCTTCTCTGTGACCTTGA		

Db 1403 GGAACATCATGTCCTCCATCAATGGCAGAGCATGAGCTTCTCTGATCACTCTGCA 1462  
QY 1544 GCGCGAGTATCTACACAAATTTCTAAGCAGCGCTCAAGCTATCTGCTGATCAAG 1603  
Db 1463 GCGCGAGTATCTACACAAATTTCTAAGCAGCGCTCAAGCTATCTGCTGATCAAG 1522  
QY 1604 CAAGCCTGTGAAGAAATACAGATATCTGAGAAATTTGCCAGAGAAATTAATGATGCA 1663  
Db 1523 CAAGCCTGTGAAGAAATACAGATATCTGAGAAATTTGCCAGAGAAATTAATGATGCA 1582  
QY 1664 ACACACAGTGAAGTGGCAGTTGCGAGAGAAAGCAAGCTCTGATGCTGAGCTTTAAA 1723  
Db 1583 ACACACAGTGAAGTGGCAGTTGCGAGAGAAAGCAAGCTCTGATGCTGAGCTTTAAA 1642  
QY 1724 AGGACATCTGTAAAGCCTGTGTCATCTATTTGAAAGAAATGTGAGACTAAATTTA 1783  
Db 1643 AGGACATCTGTAAAGCCTGTGTCATCTATTTGAAAGAAATGTGAGACTAAATTTA 1702  
QY 1784 TGGCAGCAGCAGAGGACCAATTTTGGGCGATGACATGTGTGTCGGGAGAGACAGTGTG 1843  
Db 1703 TGGCAGCAGCAGAGGACCAATTTTGGGCGATGACATGTGTGTCGGGAGAGACAGTGTG 1762  
QY 1844 TGAATATGTGTATGAAGGCGGAGCCAGCCATGGCGCATGTGTGAGCTGGTCTTCT 1903  
Db 1763 TGAATATGTGTATGAAGGCGGAGCCAGCCATGGCGCATGTGTGAGCTGGTCTTCT 1822  
QY 1904 GGTGCCCATGCTCCAGAGCTGCGAGGGGAGATATCTGATAGAGATCGCTCTGACCA 1963  
Db 1823 GGTGCCCATGCTCCAGAGCTGCGAGGGGAGATATCTGATAGAGATCGCTCTGACCA 1882  
QY 1964 ACCCCAGCGCATGCGATGAGGGGAAATTTCTGTAGGGGCTCACTCGCATCTGAACTCT 2023  
Db 1883 ACCCCAGCGCATGCGATGAGGGGAAATTTCTGTAGGGGCTCACTCGCATCTGAACTCT 1942  
QY 2024 GCAACAGTCAGAAATGTCCCGGGGACAGTGTGACTTCCGTGTGCTCAGTGTGCCAGC 2083  
Db 1943 GCAACAGTCAGAAATGTCCCGGGGACAGTGTGACTTCCGTGTGCTCAGTGTGCCAGC 2002  
QY 2084 ACAACAGCAGAGGATTCAGAGGGGCGGACATCAAGTGAAGCTTTCACTCAATGAGAG 2143  
Db 2003 ACAACAGCAGAGGATTCAGAGGGGCGGACATCAAGTGAAGCTTTCACTCAATGAGAG 2062  
QY 2144 ATCAGAGCTTTAGCAAACTCTACTGTATGCGAGAGAAATTTGATTTCTTTCTTTGT 2203  
Db 2063 ATCAGAGCTTTAGCAAACTCTACTGTATGCGAGAGAAATTTGATTTCTTTCTTTGT 2122  
QY 2204 CAATTAAGTCAAAAGATGGGACTCCATGCTCGAGGATAGCCGTATGTTTGTATGATG 2263  
Db 2123 CAATTAAGTCAAAAGATGGGACTCCATGCTCGAGGATAGCCGTATGTTTGTATGATG 2182  
QY 2264 GGAATATGAGAGAGTGTGATGCAATGTCTTGGATCTGATGCTGTGAAAGAGCTCT 2323  
Db 2183 GGAATATGAGAGAGTGTGATGCAATGTCTTGGATCTGATGCTGTGAAAGAGCTCT 2242  
QY 2324 GTGGGGTGTGTAAAGGGAATTAATCAAGCTGCGACGATTAACAGGGGTCTCTACACCAAC 2383  
Db 2243 GTGGGGTGTGTAAAGGGAATTAATCAAGCTGCGACGATTAACAGGGGTCTCTACACCAAC 2302  
QY 2384 ACCACACACCAACAGTATTTATCAATGATGATCAATGCTTCTGAGGCGGAGATATCC 2443  
Db 2303 ACCACACACCAACAGTATTTATCAATGATGATCAATGCTTCTGAGGCGGAGATATCC 2362  
QY 2444 GGAATATGAGAGAGTGTGATGCAATGTCTTGGATCTGATGCTGTGAAAGAGCTCT 2503  
Db 2363 GGAATATGAGAGAGTGTGATGCAATGTCTTGGATCTGATGCTGTGAAAGAGCTCT 2422  
QY 2504 ACTACTGATGAGGCGCTGAGCCGTGTGATGAGCCGCGCGGATCAAAATTTTGGGCGACTA 2563  
Db 2423 ACTACTGATGAGGCGCTGAGCCGTGTGATGAGCCGCGCGGATCAAAATTTTGGGCGACTA 2482  
QY 2564 CTTTGACTACAGAGGCTCTATTAATGAGCCGAGAACTTAATGCTATGAGCAACCA 2623

Db 2483 CTTTGACTACAGAGGCTCTATTAATGAGCCGAGAACTTAATGCTATGAGCAACCA 2542  
QY 2624 ACAGACACTGATTTGTGAGGCTGCTGTTTCAGGGAGGAAACCGGGGTGTGCTGGGAT 2683  
Db 2543 ACAGACACTGATTTGTGAGGCTGCTGTTTCAGGGAGGAAACCGGGGTGTGCTGGGAT 2602  
QY 2684 ACTCATGCTGTGCTTGGGAGCCGAGAAAGCAAGCCCCCTGCCCCAGCTACATTTGG 2743  
Db 2603 ACTCATGCTGTGCTTGGGAGCCGAGAAAGCAAGCCCCCTGCCCCAGCTACATTTGG 2662  
QY 2744 CCATGCTGCTCTGATGCTCCGTGCTCGGCGAGGGGG 2783  
Db 2663 CCATGCTGCTCTGATGCTCCGTGCTCGGCGAGGGGG 2702

## RESULT 13

US-10-363-937-34

Sequence 34, Application US/10363937

Publication No. US20040053269A1

GENERAL INFORMATION:

APPLICANT: Todd, Stephen; Delegeane, Angelo M.;

APPLICANT: Gandhi, Ameena R.; Nguyen, Daniel B.;

APPLICANT: Hafalia, April J.A.; Kearney, Liam;

APPLICANT: Lu, Yan; Lee, Ernestine A.;

APPLICANT: Chawla, Natinder K.; Das, Debopriya;

APPLICANT: Arvizu, Chandra S.; Yao, Monique G.;

APPLICANT: Kallick, Deborah A.; Elliott, Vicki S.;

APPLICANT: Ding, Li; Yue, Henry;

APPLICANT: Reddy, Roopa; Burford, Neil;

APPLICANT: Baughn, Mariah R.; Lal, Preeti G.;

APPLICANT: Borowsky, Mark L.; Lu, Dyrng Aina M.;

APPLICANT: Ramkumar, Dayalaxmi; Yang, Dunning;

APPLICANT: Tribouley, Catherine M.; Khan, Farrah A.;

APPLICANT: Gururajan, Rajagopal; Tang, Y. Tom;

APPLICANT: Au-Young, Janice; Warren, Bridget A.;

APPLICANT: Hernandez, Roberto; Duggan, Brendan M.

TITLE OF INVENTION: PROTEASES

FILE REFERENCE: PI-0212 USN

CURRENT APPLICATION NUMBER: US/10/363,937

CURRENT FILING DATE: 2003-03-04

PRIOR APPLICATION NUMBER: PCT/US01/28161

PRIOR FILING DATE: 2001-09-06

PRIOR APPLICATION NUMBER: US 60/231,039

PRIOR FILING DATE: 2000-09-08

PRIOR APPLICATION NUMBER: US 60/232,812

PRIOR FILING DATE: 2000-09-15

PRIOR APPLICATION NUMBER: US 60/234,850

PRIOR FILING DATE: 2000-09-22

PRIOR APPLICATION NUMBER: US 60/236,500

PRIOR FILING DATE: 2000-09-29

PRIOR APPLICATION NUMBER: US 60/238,773

PRIOR FILING DATE: 2000-10-05

PRIOR APPLICATION NUMBER: US 60/239,658

PRIOR FILING DATE: 2000-10-11

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PERL Program

SEQ ID NO 34

LENGTH: 3389

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc\_feature

OTHER INFORMATION: Incyte ID No. US20040053269A1 7478405CB1

US-10-363-937-34

Query Match 24.5%; Score 709.6; DB 18; Length 3389;

Beet Local Similarity 65.0%; Pred. No. 1.2e-212; Indels 4; Gaps 2;

Matches 1081; Conservative 0; Mismatches 579; Indels 4; Gaps 2;

Db 1124 AGACCTTGATGATGTCAGCAAAAGATGATGCAAAACCATGCGCATGAAATATCACCA 1183

Db 1096 AAACGTGTGTGTGAGACCTTAATTTCTGTGAAACAAACCTGAGATTAATGATCA 1155

QY 1184 CTTACGCTGCTACAGATCTCAACATGTGATCTGCTTTTATTCAAAGATGATGATGGGA 1243  
Db 1156 CCATCATGACAGACAGCTCTGTAATAGTTTGTG-TCAATGGCAGTGTGCCCTCATTTGAA 1214  
QY 1244 AAGATGGACTGCTGATGACCAAGCCATCTTACTGACTGCTGATATATTTTCTTGA 1303  
Db 1215 AGATGGCAAGACATGATCATGCTCATTTACTTAACAGATTTGATATTTTCTTGA 1274  
QY 1304 AGATGAGCCCTGTGACACTTTGGGATTTTGCACCCCAATGAGTATGATGATATATC 1363  
Db 1275 AGATGACCATGATGACACTCTAGGGTTTGTCCCATGATGAAATGTGCTTAAGTACC 1334  
QY 1364 GCAGTGCACGATTAATGAAGATCAAGTCTTGAGCTGAGCTTCAACATTTGCCATGAGT 1423  
Db 1335 GAAGTTGATACATCATATGAGACACAGACTTGAGCTTGTGCTTCAACATGCTCATGAGT 1394  
QY 1424 CTGGAACAACTTTTGGCATATTCATGATGAGAGAGAAACATGTATTAATAAGTCCGAGG 1483  
Db 1395 CAGGGGACAACTTTGGTATATTCACGACGAGAGAGAGAAATCCCTGCAGAAAGGCTGAG 1454  
QY 1484 GCAACATCATGTCCCTTACATTTGGCAGAGACGCAATGAGTCTTCTCTGTGCTACCCCTGCA 1543  
Db 1455 GCATATCATGTCTCCACACTGACCGGAAACATAGAGTGTTCATAGGTCTTCTCTGCA 1514  
QY 1544 GCCGCAATATCTACACAAATTTCTAAGCACCGCTCAAGCTATCTGCTTGTGATCAGC 1603  
Db 1515 GCCGCAATATCTCAAGAAATTCCTCAGCACCTCAGCGGGGTGTCTAGTGGATGAGC 1574  
QY 1604 CAAAGCTGTGAAGAAATCAAGTATCTGAGAAATTTGCCAGAGAAATTAATGATGCAA 1663  
Db 1575 CCAAGAGAGAGACATGATTAATATCCGAGCAAACTACACAGACAGATTTAATGATGCTG 1634  
QY 1664 ACACAGATGCAAGTGGCAGTGGAGAGAGAAAGCAAGCTCTGAGCTGAGCTTTTAAA 1723  
Db 1635 ACACAGATGTAATATGCAATTTGGAGCAAAAGCCAAATGATCAAGCTTGTGTTGTGA 1694  
QY 1724 AGGACATCTGTAAAGCCCTGTGTGCTGCTATGTAATGGAAGAAATGATGACTTAAATTA 1783  
Db 1695 AGGATATTTGCAATATCATTTTGTGTCACCGAGTAGGCCACAGGTGTGAGACCAAGTTTA 1754  
QY 1784 TGGCAGCAGCAAGGACCAATTTTGGGACATGACATGTGTGTCCGGGAGAGACATGTG 1843  
Db 1755 TGGCCCAAGAGAGAGGACCGTTTGTGCTTGAATGTGTGTCCGCAAGGCAAGTGTGCG 1814  
QY 1844 TGAATATGTGTATGAAGGCCCAAGGCCCAACCATGAGCCATGAGTGTGCTTCTT 1903  
Db 1815 TAAAGTTTGGGAGCTGCGGCCCGGCCCATTCACGAGCATGTGTGCTGCTGTGCAAGT 1874  
QY 1904 GGTCCCATGTCTCAGAGCTGTGCGAGGGGAGATATCTCATAGAGTCCGCTTGCACCA 1963  
Db 1875 GGTCAAAATGTTCCCGGACATGTGTGAGAGAGTCAAGTTCCAGAGAGACACTGCAATA 1934  
QY 1964 ACCCAAGCATGATGAGAGGAGATTTCTGTAGGGCTTCACTCGCACTTGAAGTCT 2023  
Db 1935 ACCCAAGCTCAATGTGTGTGATATTTCTGTCAAGTCTTACCGTATTTATCACTGT 1994  
QY 2024 GCAACAGTCAAAATGTCGCCCGGACAGTGTGATCTTCCGTGTGCTCAGTGTGCGAGC 2083  
Db 1995 GCATATTTAACTCTTGCATGAAATTAAGCTTGAATTTTGGGCTCAACAGTGTGCAAGAT 2054  
QY 2084 ACAACAGCAGACGATTCAGAGGCGGACATCAAGTGAAGCTTCACTCACTCAAGTGAAG 2143  
Db 2055 ATAAAGCAAACTTTCCGTGATGGTTCTTACAGAGTGAAGCCCTTAACAAAGTGGAG 2114  
QY 2144 ATAGAGCTTATGCAACTTACTGTATCGCAGAGAGATTTGATTTCTTTCTTTTGT 2203  
Db 2115 AGGAAATGATCACTCAACTGTACTGCAAGCTGAGAACTTTGAAATTTTGTTCATGT 2174  
QY 2204 CAAATTAAGTCAAAAGTGGGACTCAATGCTCGAGAGATGCGGTATATGTTTGTATGATG 2263  
Db 2175 CCGGCAAAAGTGAAGATGAACTCCCTGCTCCCAACAAATTAATGATTTGATGAGC 2234  
QY 2264 GGATATGTGAGAGATTTGATGACATGTCTTGGATCTGATGTGTGGAAGCGTCT 2323

Db 2235 GGGTTGTGAACATAGTGGAGTGTGATCATGAACCTAGCTCTAAAGCATTTTCAGATGCTT 2294  
QY 2324 GTGGGGTGTGTAACGGGAATPACTCAGCCGCAAGTTCACAGGGGCTCTACACAGC 2283  
Db 2295 GTGGCGTTTGCAAGGATGATTAATCACTTGCAAGTTTATTAABGCCGTGATCTTAAC 2254  
QY 2384 ACCACCAACCAACAGATTAATCAATGATGACCAATTCCTTGTGAGCCCGAGATATCC 2443  
Db 2355 AGCATTAACCAATTAATTAATCCGTGTATCATTTCACTGAGTGGCGCCGAAGCATG 2414  
QY 2444 GCATCTATGAATGAACGTCTTACTCTTCACTTTCTGTGCAATGCCCTCAGAGT 2503  
Db 2415 AATCCAGAGCTGCGAGTGTTCCTCAGTTACTCTCAGTTGAGAGCTCAATCAAAAGT 2474  
QY 2504 ACTACCTGAATGGGACCTGAGCCGTGACCTGGCCCGCGCGGATCAAAATTTTGGGACAT 2563  
Db 2475 ATTACCTCACCGGGGCTGAGCATGACTGGCTGGGGAGTTCCCTTGTGCGGAGCA 2534  
QY 2564 CTTTCACTACAGACGGTCTATTAATGAGCCCGAAGAACTTAATCGCTACGACCAACA 2623  
Db 2535 CGTTGAATACAGCGCTCTTTCAACCGCCGGAAGTCTGTACGGCCAGGCGCAACA 2594  
QY 2624 ACAGACACTGATTTGTGAGCTGTGTTTCAAGGAAAGAACCCGGGTGTGCTGGAAT 2683  
Db 2595 ATGAGACGCTGCTTTGAAATTTCTGATGCAAGCAAAATCAGAGGATGATTTGGAAGT 2654  
QY 2684 ACTCCATGCTGCTGGGAGCCGAGAACAGCCCCCTGCGCA--GCCAGCTACACTT 2740  
Db 2655 ATGCACTTCCCAAGGTCATGAATGAACTCACACAGCCCAAAAGAACCTGCTTATACCT 2714  
QY 2741 GGGCATCGTGGCTGTGAGTGTCCGTGCTGCGAGAGGGGT 2784  
Db 2715 GGAATATCGTGCAGTCAAGTGTCTCGTCTCTGTGTGTGAAGT 2758

RESULT 14  
US-10-354-983-3  
; Sequence 3, Application US/10354983  
; Publication No. US2004004194A1  
; GENERAL INFORMATION:  
; APPLICANT: ACOSTINO, MICHAEL J.  
; APPLICANT: CORCORAN, CHRISTOPHER  
; TITLE OF INVENTION: AGRECEANASE MOLECULES  
; FILE REFERENCE: 08702.0111-00000  
; CURRENT APPLICATION NUMBER: US/10/354,983  
; CURRENT FILING DATE: 2003-01-31  
; PRIOR APPLICATION NUMBER: 60/353,680  
; PRIOR FILING DATE: 2002-01-31  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 3219  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-354-983-3

Query Match 24.5%; Score 708; DB 18; Length 3219;  
Best Local Similarity 64.9%; Pred. No. 3.8e-212;  
Matches 1080; Conservative 0; Mismatches 580; Indels 4; Gaps 2;  
QY 1124 AGACCTGTGTGTGTGTCGACAAAGATGATCAAAACATGAGCCATGAATATATACCA 1183  
Db 945 AAACGTGTGTGTGTGAGGCTTAATTTCTTGAACAAAGAACTGAGAGTTATGATCA 1004  
QY 1184 CTTAGCTGTCAAGATCACTCAATGATATGCTTTATTTCAAGATGATGATGAGGA 1243  
Db 1005 CCATCATGACAGCAAGTCTCTGAATAGTTTGTG-TCAATGGCAGTGTGCCCTCATTTGAA 1063  
QY 1244 AAGATGGACTGCTGATGACAGCGCATTTTACTGACTGTCTGATATATGTTCTTGA 1303  
Db 1064 AAGATGGCAAGAGACATGATCATGCTATCTTAACAGATTTGATATTTTCTTGA 1123



QY 1424 CTGGACACAACTTTGGCATGATTCATGATGAGAGAGGAAACATGTGTAAAAAGTCCGAGG 1483  
 DB 1313 CAGGGGACAACTTTGGTATGATTCACGACGGAGAGAGGAAATCCCTCAGAAAAGCTGAAG 1372  
 QY 1484 GGAACATCATGTCCTTACATTTGGCAGAGAGCAATGAGTCTTCTCTGTCACTGTCA 1543  
 DB 1373 GCATATCATGTCCTTCCACACGACCGGAAACATGAGTGTTCATGTCTTCTTGA 1432  
 QY 1544 GCGCAGATATCTACACAAATTTCTAAGCACCGCTCAAGCTATCTGCTTGCATGACG 1603  
 DB 1433 GCGCAGATATCTACAGAAATTTCTCAGCACACCTCAGCGGGGTGTCTAGTGAATGAGC 1492  
 QY 1604 CAAAGCTGTGAAGAAATACAGATATCTGAGAAATTTCCAGAGAAATTAATGATGCA 1663  
 DB 1493 CCAAGCAAGAGAGAGATTAATATCCGGAACAACTACAGAGACAGATTAATGATGCTG 1552  
 QY 1664 ACACACAGTGCAGTGGCAGTTCGAGAGAAAGCAAGCTCTGCAATGCTGGAATTTAAA 1723  
 DB 1553 ACACACAGTGAATGAGCAATTTGAGCAAAAGCCAAAGTATGACACCTTGTGTGTA 1612  
 QY 1724 AGGACATCTGTAAAGCCCTGTGTCATGTAATTTGAAAGAAATGAGACTAAATTTTA 1783  
 DB 1613 AGGATATTTGCAAAATCACTTTGTCACGAGTAAGCCACAGGTGTGAGACCAAGTTTA 1672  
 QY 1784 TGCACAGCAGAGAGAGCACAATTTGTGGCATGACATGTGTGTCGAGAGAGCAAGTGTG 1843  
 DB 1673 TGCCTCGACAGAGAGAGAGCGTTGTGTGTGATGATGTGTGTGCGCAAGGCAAGTGTG 1732  
 QY 1844 TGAATATGTGTGAAGGCCCCCAAGCCCACTGAGCCACTGTGCACTGTCTTTCTT 1903  
 DB 1733 TAAAGTTTGGGAGCTCGGGCCCCGCCATCCACGCGCAGTGTCTGCTGTGTGCAAGT 1792  
 QY 1904 GGTCCCATGCTCTCAGAGACCTGCGAGGGGAGTATCTCATAGAGTCCGCTGTGCACCA 1963  
 DB 1793 GGTCAAGATGTTTCCGAGACATGTGTGAGAGAGTCAAGTTCCAGAGAGACACTGCAATTA 1852  
 QY 1964 ACCCAAGCCATCGCATGAGAGGAGTCTGTGAGGGCTCCACTGCACTGTGAAGCTCT 2023  
 DB 1853 ACCCAAGCCCTCGATGTGTGCGATATTTCTGTCCAGGTTCTAGCCGATTTATCACTGT 1912  
 QY 2024 GCACAGTCAAGAAATGTCCTCCGAGAGAGTGTGATTTCCGTGCTGCTCAATGTCCGAGC 2083  
 DB 1913 GCATATTTAACTCTTCAATGAAATAGCTTGTGATTTTCCGGCCCAACAGTGTGCAAGT 1972  
 QY 2084 ACAACAGCAGACGATTCAGAGGGGCGACATAAGTGAAGCCTTACACTCAAGTAGAAG 2143  
 DB 1973 ATTAACGCAAACTTTCCGTGATGTTCTTACAGATGGAACCTTATCAAAAGTGAAG 2032  
 QY 2144 ATCAGGACTTATGCAAACTCTACTGTATCGCAGAGAGATTTGAATTTCTTTCTTTGT 2203  
 DB 2033 AGGAGATGAGTCAAACTGTACTGCAAGCTGAGAACTTTGAATTTTTTTTGTGCAATGT 2092  
 QY 2204 CAAATTAAGTCAAAAGTGGAGTCTCATGCTCGAGAGATAGCCGTAAATGTTGTATAGATG 2263  
 DB 2093 CCGGCAAGTGAAGATGGAATCCCTGCTCCCAACAGAAATGATGTTGTATGAGC 2152  
 QY 2264 GGATATGTGAGAGATGATGATGCAATGCTTGTGATCTGATGCTGTGTAAGAGTCT 2323  
 DB 2153 GGGTTTGTGAATGAGTGTGATGATGATCACTAGGCTTTAAGGAGTTTCAAGTCTT 2212  
 QY 2324 GTGGGTGTGTAACTGGGAAATTACTCAGGCTGACGATTCAGAGGGTCTTACACCAAGC 2383  
 DB 2213 GTGGCGTTTGGCAAGGTGATTAATTAAGTTTGAAGGCTGTACCTCAACC 2272  
 QY 2384 ACCACACACCAACGATATTAATCAATGTCACATTCCTTGTGAGCCCGAGATATCC 2443  
 DB 2273 AGCATTAAGCAATGATATTAATCCGATGTCATCAATCCAGCTGCGCCGCAAGCATCG 2332  
 QY 2444 GCATCTATGAAATGAAGTCTACCTACCTACATTTCTGTGAGCAATGCCCCCAGAAAGT 2503  
 DB 2333 AAATTCAGAGGCTGCGGTTTCTCCAGTTTACCTCGAGTTTGAAGCCTCAGTCAAAAGT 2392  
 QY 2504 ACTACTGAATGGGCACTGGACCGTGAATGCGCCGCGTACAAATTTTCCGGGACATA 2563

DB 2393 ATTAACCTCACCGGGGCTGGAGCATGAGCTTGGGAGATTCCCTTGTGAGGACCA 2452  
 QY 2564 CTTTGACATACAGACGCTCTAATATGAGCCCGAGAACTTAATCGCTACGTGACCAACCA 2623  
 DB 2453 CTTTGAATACAGACGCTCTTTCACCCCGGAACTGTATGAGGCAAGGCCACAA 2512  
 QY 2624 ACAGACACTGATTTGTGAGCTGTGTTTCAAGGAAAGAACCCGGGTGTTGCTTGGAAAT 2683  
 DB 2513 ATGAGACGCTGGTCTTTGAATTTCTGATGCAAGCAAAATATCAGGATAGCTTGAAGT 2572  
 QY 2684 ACTCATGCTTGTGCTTGGGAGCCGAGAGACAGCCCCCTGCCA--GCCAGCTTACATT 2740  
 DB 2573 ATGCACTTCCCAAGGTCAATGAATGGAATCCACAGCCCAAAAGAACCTGCTATATCT 2632  
 QY 2741 GGGCCATCGTGGGCTCTGAGTGTCCGTGCTGCGGAGGGGCT 2784  
 DB 2633 GAGATATGATGAGTGTGAGTGTCTGCTGCTGTGTGTGAGGT 2676

Search completed: September 9, 2005, 22:16:19  
 Job time : 1740 secs

This page Blank (uspb)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2005, 02:13:13 / Search time 492 Seconds  
(without alignments)  
9628.092 Million cell updates/sec

Title: US-09-981-151D-7  
Perfect score: 2895  
Sequence: 1 cgcctcgcagtcgagcccg.....ccccgggcttcctcccgca 2895

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/prodata/1/ina/5A COMB.seq: \*  
2: /cgn2\_6/prodata/1/ina/5B COMB.seq: \*  
3: /cgn2\_6/prodata/1/ina/6A COMB.seq: \*  
4: /cgn2\_6/prodata/1/ina/6B COMB.seq: \*  
5: /cgn2\_6/prodata/1/ina/PCFUS COMB.seq: \*  
6: /cgn2\_6/prodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1874.6	64.8	3675	3	US-09-930-872-3	Sequence 3, App1
2	1874.6	64.8	3675	4	US-10-217-774-3	Sequence 3, App1
3	1874.6	64.8	4042	4	US-09-930-872-5	Sequence 5, App1
4	1874.6	64.8	4042	4	US-10-217-774-5	Sequence 5, App1
5	663	22.9	1476	3	US-09-930-872-1	Sequence 1, App1
6	663	22.9	1476	4	US-10-217-774-1	Sequence 1, App1
7	227	7.8	2274	4	US-09-963-791-23	Sequence 23, App1
8	227	7.8	2274	4	US-09-963-791-1	Sequence 1, App1
9	209.6	7.2	3571	4	US-09-799-451-411	Sequence 411, App1
10	206.4	7.1	3377	4	US-09-981-953A-3	Sequence 3, App1
11	204.6	7.1	5357	3	US-09-392-184-5	Sequence 5, App1
12	201.6	7.0	3766	4	US-09-981-953A-1	Sequence 6, App1
13	182.6	6.3	3218	3	US-09-369-364A-6	Sequence 16, App1
14	176.8	6.1	3885	3	US-09-369-364A-16	Sequence 16, App1
15	144	5.0	2848	3	US-09-369-364A-4	Sequence 2, App1
16	123	4.2	3160	4	US-09-963-791-25	Sequence 25, App1
17	118.4	4.1	2450	3	US-09-491-522-2	Sequence 2, App1
18	118.4	4.1	6592	3	US-09-491-522-1	Sequence 1, App1
19	118	4.1	1317	4	US-09-963-791-21	Sequence 21, App1
20	118	4.1	1770	4	US-09-963-791-11	Sequence 11, App1
21	116.8	4.0	3656	3	US-09-949-016-5530	Sequence 5530, App1
22	114.2	3.9	2450	3	US-09-491-522-9	Sequence 9, App1
23	114.2	3.9	4580	3	US-09-491-522-8	Sequence 8, App1
24	113.6	3.8	5804	3	US-09-369-364A-12	Sequence 12, App1
25	110	3.5	2853	4	US-10-009-332-2	Sequence 2, App1
26	102.6	3.5	1071	4	US-09-963-791-19	Sequence 19, App1
27	102.6	3.5	1534	4	US-09-963-791-9	Sequence 9, App1

28	102.4	3.5	3002	3	US-09-369-364A-1	Sequence 1, App1
29	101.2	3.5	2184	4	US-09-445-023A-13	Sequence 13, App1
30	97.2	3.4	3706	3	US-09-484-970B-58	Sequence 58, App1
31	97.2	3.4	4676	3	US-09-130-491-1	Sequence 1, App1
32	97.2	3.4	4676	3	US-09-392-184-1	Sequence 1, App1
33	95.6	3.3	3889	4	US-09-568-559-1	Sequence 1, App1
34	94	3.2	2184	4	US-09-445-023A-2	Sequence 2, App1
35	91.6	3.2	954	4	US-09-963-791-15	Sequence 15, App1
36	91.6	3.2	1407	4	US-09-963-791-5	Sequence 5, App1
37	85.4	2.9	6659	4	US-09-321-987B-1	Sequence 1, App1
38	85.2	2.9	2625	3	US-09-369-364A-14	Sequence 14, App1
39	85.2	2.9	3638	3	US-09-369-364A-8	Sequence 8, App1
40	83.6	2.9	3250	3	US-09-122-126B-14	Sequence 14, App1
41	83.6	2.9	3250	4	US-09-634-286A-14	Sequence 14, App1
42	83.6	2.9	3250	4	US-10-247-685-14	Sequence 14, App1
43	80.4	2.8	601	4	US-09-949-016-164396	Sequence 164396, A
44	80.4	2.8	56147	4	US-09-949-016-16352	Sequence 16352, A
45	80.4	2.8	298336	4	US-09-949-016-16600	Sequence 16600, A

ALIGNMENTS

```
RESULT 1
US-09-930-872-3
; Sequence 3, Application US/09930872
; Patent No. 6448388
; GENERAL INFORMATION:
; APPLICANT: Fildale, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. 6448388e1 Human Proteases and Polynucleotides Encoding the San
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/09/930,872
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3675
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-872-3

Query Match      64.8%; Score 1874.6; DB 3; Length 3675;
Best Local Similarity 84.4%; Pred. 1874.6;
Matches 2287; Conservative 0; Mismatches 179; Indels 245; Gaps 6;

QY      202 GCAGGACCTGCGTGCATGCGACCGCAGCGGCGCGCTGGAGCCCGAGCGTCC 261
        |||||
DB      69 GCGGACCTGCGTGCATGCGACCGCAGCGGCGCGCTGGAGCCCGAGCGTCC 128

QY      262 GCGTCTCTCTCCACCGCGGAGCGCGGCTGGATGAAAGGCGGACATGATGAA 321
        |||||
DB      129 GCGTCTCTCTCCACCGCGGAGCGCGGCTGGATGAAAGGCGG----- 175

QY      322 GCGGAAACATGTTCTGAGCAATCAACAGAAACAGAAACAAACATGATGTT 381
        |||||
DB      176 ----- 175

QY      382 CTCACATATATGACCTGCTCTGCGCTTACGAGTTGACACAGGCGGATTAAGTCTCC 441
        |||||
DB      176 -----AATATGACCTGCTCTGCTTACGAGTTGACACAGGCGGATTAAGTCTCC 228

QY      442 CATGAATCATGACATCATGAGCGCGGAGAAAGACGATGCGCTTCCAGTTGATGCT 561
        |||||
DB      229 CATGAATCATGACATCATGAGCGCGGAGAAAGACGATGCGCTTCCAGTTGATGCT 288

QY      502 CTCACCTTGGTGGTGAAGGCCCGAGGACGACCTTCAATGATGATGAGACTTCAGC 561
        |||||
DB      289 CTCACCTTGGTGGTGAAGGCCCTTCAGGACGACCTTCAATGATGATGAGACTTCAGC 348

QY      562 AGCTATGAGCTCTCGCTTATTTGTCAGACGTTGGAAAGACAGGACCTAAGTCTGTG 621
```



Db 349 AGCTATGCTGCTCTGCTTATTTGTCACAGCTGGGAAAGACAGCACTTAAGTCTGTG 408  
QY 622 CAGACTTTACCGCCAGAGAGCTTCTGTTTCTATCAAGGCTCTTTGGCATCACAGAAAC 681  
Db 409 CAGACTTTACCGCCAGAGAGCTTCTGTTTCTATCAAGGCTCTTTGGCATCACAGAAAC 468  
QY 682 TCGCCATCGCATGAGGAAAGTTCTGTGAGGGCTCCACTGCACTCTGAAGCTCTGCAAC 741  
Db 469 TCTCTCA-----GTGGCCCTTTCAACCTGCCAAAGCTTGTC 504  
QY 742 AGTCAGAAATGTCCCGGAGCAGTTGTGACTTCGTGCTGCTCAAGTGTGCCAGCAAC 801  
Db 505 GGCATGTTACCAACAGAAAGGAGATTACTTCTTAAGGCCACTTCTTCAACCTCTCA 564  
QY 802 AGCAGAGATTGAGAGGGCCGCACTCAAGTGG--AAGCTTACACTCAAGTGAAGCCG 859  
Db 565 TGGAACTGGCAGAGAGCTGCCCAAGGAGCTCGGCATCCACGTACTGTACAAAGATCC 624  
QY 860 ACTTATGCAAACTCTACTGTATGTGCAGAAAGATTGATTTCTTTCTTTCTTTGCAAAAT 919  
Db 625 ACAGAGCCCATGCTCTCTGGGGCAGTGAAGTCTGTGACTC-----AAGG 672  
QY 920 AAGTCAAAAGTGGGACTCCATGCTCGGAGGATAGCCGTATGTTGTATATAGATGGATAT 979  
Db 673 ACATGGAGCTGGCAATCAACCCCTGCACAGAGCGACTTGCCTGGGACTGCCACA 732  
QY 980 GTGAGCTCAGTGTGTGTCCACATCTGC--GCATGCCCCAGGCTCCCAAGAAAGACTTC 1038  
Db 733 AAGCAGATTTCTGTGGAAGAGCAAGAAATACATGCCCGAGCTCCCAAGAAAGACTTC 792  
QY 1039 TTCTATCTTGCAGATGATATAGTCTTGTCTTAAGCGATTAAGCGCTCTCTTCTGAGTCC 1098  
Db 793 TTCTATCTTGCAGATGATATAGTCTTGTCTTAAGCGATTAAGCGCTCTCTTCTGAGTCC 852  
QY 1099 CATAGAAATGAAAGCTGAACGTGAGAGCCTTGTGTGTGTGCAAAAAAGATGATGCA 1158  
Db 853 CATAGAAATGAAAGCTGAACGTGAGAGCCTTGTGTGTGTGCAAAAAAGATGATGCA 912  
QY 1159 AACCATGGCCATGAAATATACACACTTACGTGCTCAGATTACTCAACATGATATGCT 1218  
Db 913 AACCATGGCCATGAAATATACACACTTACGTGCTCAGATTACTCAACATGATATGCT 972  
QY 1219 TTAATCAAGA----- 1229  
Db 973 TTAATCAAGAATGAACAATAGGAGAAACATCAATTGCAATTGTAGTCTGATTTCTT 1032  
QY 1230 ----- 1229  
Db 1033 CTAGAAAGATGAACGCCAGAGCTGTGATTAAGTCAACGACAGCAACCTTAAGTACG 1092  
QY 1230 -----TGGATTGATGGGAAAGATGGGACTGTGATGACCAACGCGCATC 1272  
Db 1093 TTCTGCAATGGCAGTCTGGAATTGATGGGAAAGATGGGACTGTGATGACCAACGCGCATC 1152  
QY 1273 TTAATCAAGTGTGTGATATATGTTCTCTGGAAGATGAAGCCCTGTGACACTTTGGGATTT 1332  
Db 1153 TTAATCAAGTGTGTGATATATGTTCTCTGGAAGATGAAGCCCTGTGACACTTTGGGATTT 1212  
QY 1333 GCACCCATTAAGTGAATGTGTAGTAAATATGCAAGCTGACAGATTAATAAGATACAGGT 1392  
Db 1213 GCACCCATTAAGTGAATGTGTAGTAAATATGCAAGCTGACAGATTAATAAGATACAGGT 1272  
QY 1393 GTTGAAGTGGCTTCAACATTTGCCATGAGTGTGACACAACTTTGGCATGATTCATGAT 1452  
Db 1273 GTTGAAGTGGCTTCAACATTTGCCATGAGTGTGACACAACTTTGGCATGATTCATGAT 1332  
QY 1453 GGAAGAGGAACTGTGTAAAAAGTCCGAGGGCAATCATGTCCCTTCAATTTGGCAGGA 1512  
Db 1333 GGAAGAGGAACTGTGTAAAAAGTCCGAGGGCAATCATGTCCCTTCAATTTGGCAGGA 1392  
QY 1513 GCGAATGAGTCTTCTCTGTGTCAACCTGACCGCGCATGTATCTACAAATTTCTAAGC 1572  
L 1

Db 1393 GCGAATGAGTCTTCTCTGTGTCAACCTGACCGCGCATGTATCTACAAATTTCTAAGC 1452  
QY 1573 ACCGCTCAAGCTATCTGCTTCTGTATGACGCAAAAGCCTGTGAAGAAATACAATATCT 1632  
Db 1453 ACCGCTCAAGCTATCTGCTTCTGTATGACGCAAAAGCCTGTGAAGAAATACAATATCT 1512  
QY 1633 GAGAAATTTGCCAGAGAAATTAATATATGCAAAACACAGTGTCAAGTGTGCAATTTCCGAGAG 1692  
Db 1513 GAGAAATTTGCCAGAGAAATTAATATATGATGCAAAACACAGTGTCAAGTGTGCAATTTCCGAGAG 1572  
QY 1693 AAAAGCAAGCTGTGATGTGCACTTTAAAAAGACATCTGTAAAGCCCTGTGAGCCAT 1752  
Db 1573 AAAAGCAAGCTGTGATGTGCACTTTAAAAAGACATCTGTAAAGCCCTGTGAGCCAT 1632  
QY 1753 CGTATTTGAGAGAAATGTGAGACTTAATTTATGCAAGAGCAGAAAGCAATTTGTGGG 1812  
Db 1633 CGTATTTGAGAGAAATGTGAGACTTAATTTATGCAAGAGCAGAAAGCAATTTGTGGG 1692  
QY 1813 CATGACATGTGTGCTCCGGGAGAGACAGTGTGTGAATATGTGATGAAGGCCCAAGCCC 1872  
Db 1693 CATGACATGTGTGCTCCGGGAGAGACAGTGTGTGAATATGTGATGAAGGCCCAAGCCC 1752  
QY 1873 ACCCATGGCACTGGTCGGAATGTGCTTCTTGTGCCATGCTCCAGACCTTGGAGGG 1932  
Db 1753 ACCCATGGCACTGGTCGGAATGTGCTTCTTGTGCCATGCTCCAGACCTTGGAGGG 1812  
QY 1933 GAGATATCTCATAGGAGTGCCTCTGCAACCAACCCCAAGCCATCGCATGAGAGGAATTC 1992  
Db 1813 GAGATATCTCATAGGAGTGCCTCTGCAACCAACCCCAAGCCATCGCATGAGAGGAATTC 1872  
QY 1993 TGTGAGGCTCCACTGTGCACTGTGAAGCTCTGCAACAGTCAGAAATGTCTCCGGGACAT 2052  
Db 1873 TGTGAGGCTCCACTGTGCACTGTGAAGCTCTGCAACAGTCAGAAATGTCTCCGGGACAT 1932  
QY 2053 GTTGACTTCCGTCGTCTCAGTGTGCGAGCAACACAGACGATTAAGAGGGGGCAC 2112  
Db 1933 GTTGACTTCCGTCGTCTCAGTGTGCGAGCAACACAGACGATTAAGAGGGGGCAC 1992  
QY 2113 TACAAGTGAAGCCTTACACTCAAGTAGAAGATCAGACTTAATGCAAACTTACTGTATC 2172  
Db 1993 TACAAGTGAAGCCTTACACTCAAGTAGAAGATCAGACTTAATGCAAACTTACTGTATC 2052  
QY 2173 GCAGAAAGATTTGATTTCTTCTTTTGTGCAATAAAGTCAAAAGATGGGACTCATGC 2232  
Db 2053 GCAGAAAGATTTGATTTCTTCTTTTGTGCAATAAAGTCAAAAGATGGGACTCATGC 2112  
QY 2233 TCGAGAGATGACCGTAATGTTGTATAGATGGGATATGAGAGGTTGATGTGACAT 2292  
Db 2113 TCGAGAGATGACCGTAATGTTGTATAGATGGGATATGAGAGGTTGATGTGACAT 2172  
QY 2293 GTCTTTGATCTGATGCTGTGGAAGCGTCTGTGGGTGTGTAAACGGGAATTAATCAGCC 2352  
Db 2173 GTCTTTGATCTGATGCTGTGGAAGCGTCTGTGGGTGTGTAAACGGGAATTAATCAGCC 2232  
QY 2353 TGCAGATTTCAAGGGGTCTCTACACCAAGCAACCAACCAAGATTAATCAATG 2412  
Db 2233 TGCAGATTTCAAGGGGTCTCTACACCAAGCAACCAACCAAGATTAATCAATG 2292  
QY 2413 GTCAACATTTCTTCTGAGACCGGAGTATCGGCACTTAATGAATGAAGTCTTCACTCC 2472  
Db 2293 GTCAACATTTCTTCTGAGACCGGAGTATCGGCACTTAATGAATGAAGTCTTCACTCC 2352  
QY 2473 TACATTTTGTGTGCGAATGCCCTCAGAAAGTATCACTGAAATGGGCACTGACCGTGGAC 2532  
Db 2353 TACATTTTGTGTGCGAATGCCCTCAGAAAGTATCACTGAAATGGGCACTGACCGTGGAC 2412  
QY 2533 TGGCCCGGCGGTACAAATTTTGGGCACTTTCGACTACAGCGGTCTTATATAG 2592  
Db 2413 TGGCCCGGCGGTACAAATTTTGGGCACTTTCGACTACAGCGGTCTTATATAG 2472  
QY 2593 CCCGAGAACTTAATGTGCTACTGAGCAACCAAGCAACGACATGATTTGGAGCTGTGTT 2652  
Db 2473 CCCGAGAACTTAATGTGCTACTGAGCAACCAAGCAACGACATGATTTGGAGCTGTGTT 2532

Qy	2653	CAGGGAAGGAACCCGGGAGTGTGCTGGGAAATACTCCATGCTCGCTTGGGACCGAGAAG	2712
Db	2513	CAGGGAAGGAACCCGGGAGTGTGCTGGGAAATACTCCATGCTCGCTTGGGACCGAGAAG	2592
Qy	2713	CAGCCCCCTGGCCAGGCCAGCTACACTTGGGSCATCGGCGCTCTGAATGCTCCGTGTCC	2772
Db	2593	CAGCCCCCTGGCCAGGCCAGCTACACTTGGGSCATCGGCGCTCTGAATGCTCCGTGTCC	2652
Qy	2773	TGCGGAGGGGG	2783
Db	2653	TGCGGAGGGGG	2663

RESULT 2  
US-10-217-774-3  
; Sequence 3, Application US/1021774

```

? Patent No. 6734007
? GENERAL INFORMATION:
? APPLICANT: Fiddie, Carl Johan
? APPLICANT: Hildun, Erin
? TITLE OF INVENTION: No. 6734007/1 Human Proteases and Polynucleotides Encoding the
? TITLE OF INVENTION: Same
? FILE REFERENCE: LEX-0219-USA
? CURRENT APPLICATION NUMBER: US/10/217,774
? CURRENT FILING DATE: 2002-08-12
? PRIOR APPLICATION NUMBER: US/09/930,872
? PRIOR FILING DATE: 2001-08-14
? PRIOR APPLICATION NUMBER: US 60/225,852
? PRIOR FILING DATE: 2000-08-16
? NUMBER OF SEQ ID NOS: 5
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 3
? LENGTH: 3675
? TYPE: DNA
? ORGANISM: homo sapiens
? US-10-217-774-3

```

Query Match	64.8%	Score 1874.6	DB 4	Length 3675
Best Local Similarly	84.4%	Pred. No. 0		
Matches 2287; Conservative	0	Mismatches 179;	Indels 245;	Gaps 6;

Qy	202	GCAGGCACTCGTGCCTCATGGGACC	CGCAGCGCAGCGCTGGGAACCCGAGCGTCC	261
Db	69	GCAGGCACTCGTGCCTCATGGGACC	CGCAGCGCAGCGCTGGGAACCCGAGCGTCC	128
Qy	262	GCCTTCCTCTCCACCCCGGAGCGGCGCGGCTGGATGGAAAAAGCGGAGCATGGATGAA		321
Db	129	GCCTTCCTCTCCACCCCGGAGCGGCGCGGCTGGATGGAAAAAGGCGG		175
Qy	322	GCTGGAAACATCGTCTCAGCAAACTAACA	CAGGAAACAGAAAACMAAACCTGCATGTT	381
Db	176	-----	-----	175
Qy	382	CTCACTCAATATGACCTGTGCTCTGCCTACAGAGTTGACCA	CAGGGCGAATTAACGTGCC	441
Db	176	-----AAATATGACCTGTGCTCTGCCTACAGAGTTGACCA	CAGGGCGAATTAACGTGCC	228
Qy	442	CATGAATATCAGCAACCATCAGCGGCGGAGGAAGAGCAGTGGCGGTCTCCGAGTTGAGCT		501
Db	229	CATGAATATCAGCAACCATCAGCGGCGGAGGAAGAGCAGTGGCGGTCTCCGAGTTGAGCT		288
Qy	502	CTTGACCTTCGGCTGAAAAGGCCAGCAGCAGACTTCCACATGATCTTGAGGACTTCCAGC		561
Db	289	CTTGACCTTCGGCTGAAAAGGCCAGCAGCAGACTTCCACATGATCTTGAGGACTTCCAGC		348
Qy	562	AGCCTAGAGGCTCCGCGCTTTATTTGTGAGACGTTGGAAAAGACAGGACCTTAAGTCTGTG		621
Db	349	AGCCTAGAGGCTCCGCGCTTTATTTGTGAGACGTTGGAAAAGACAGGACCTTAAGTCTGTG		408
Qy	622	CAGACTTTAACCGCCAGAGAGCTTCTGTTTCTATCAAGGCTCTTTCGATCCACAGAAAC		681
	409	CAGACTTTAACCGCCAGAGAGCTTCTGTTTCTATCAAGGCTCTTTCGATCCACAGAAAC		468

QY	682	TCGCCATCGCATGGAGGGAGAGTTCTTGAGGGCTTCACCTCGACCTCTGAAGCTCTGCAC	741
Db	469	TCCTCA-----GTGGCCCTTTCACCTGGCCAGGCTTGTC	504
QY	742	AGTCAGAAATGTCCTCCCGGACAGGTGTGACTTCCTCGTGTCTCAAGTGTGCCGAGACAAAC	801
Db	505	GGCATGATACAGAAAGAGAGGACAGATTACTCTTAAGGCCACTTCCTTCACACCTCTCA	564
QY	802	AGCAGACGATTCAGAGGGCGGCACTACAAGTGG--AAGCTTACACTAAGTAGAAGCCG	859
Db	565	TGGAACTCGGACAGCTGCCCAAGGACAGCTCGGCATCCACGTAAGTCTTAACAAAGATCC	624

Db 625 ACAGAGCCCATGCTCTGGGGGCGAGTGGGTCTCTGTACCTC-----AAGG 672

QY	920	AAGTCAAGATGGGAGCTTCATGCTCGAGAGTAGCCGTAATGTTTGATTAATGGGATAT	979
Db	673	ACATGGAGCTCGGCATCATCAACCCCTGCACACGACGACCTTGGCCTGGGACTGCACAA	732
QY	980	GTGAGCTCATGTGTGTCTCATATCTGC-GCAATGCCCAAGCTCCCAAGAAAGCTC	1038
Db	733	AAGCAGCATTTCTCTGGGAAGAAGCAAGAAATATATGCCCCAGCCTCCCAAGAAAGCTTC	792
QY	1039	TTCATCTTGCAGATGAGATATATAGCTTGTGCTTAAGGCAATTAAGCGTCTCTTCTGAGTCC	1096
Db	793	TTCATCTTGCAGATGAGATATATAGCTTGTGCTTAAGGCAATTAAGCGTCTCTTCTGAGTCC	852
QY	1099	CATGAAATGAAAGAACTGAACGTGAGACCTTGGTGGTGTGCACAAAAGATGATGCA	1155
Db	853	CATGAAATGAAAGAACTGAACGTGAGACCTTGGTGGTGTGCACAAAAGATGATGCA	912
QY	1159	AACCATGGCCATGAAATATATCACCACCTAGCTGCTCAGATACTCAACATGTATCTGCT	1218
Db	913	AACCATGGCCATGAAATATATCACCACCTAGCTGCTCAGATACTCAACATGTATCTGCT	972

Db 973 TTATTCAAAGATGGAACAATAGGAGAAACATCAACATTGCCAATTGTAAGTCTGATTCTT 1032

Oy	1230	-----	1229
Db	1033	CTAAGATGAACGCCAGACCTGTGATTAAGTACCAACGAGACCAACACTTAAATAGC	1092
Oy	1230	-----TGATTAATGGGGAAGATGGGACTCGTCATGACCAAGCCATC	1272
Db	1093	TTCTGCGAGTGCGAGCTCTGGATTAATGGGGGAAATGGGACTCTGTATGACCAAGCCATC	1152
Oy	1273	TTACTGACTGTCTGATATATATGTTCCGGAAGATGAGCCCTGTGACACTTTGGGATTT	1332
Db	1153	TTACTGACTGTCTGATATATATGTTCCGGAAGATGAGCCCTGTGACACTTTGGGATTT	1212
Oy	1333	GCACCCATTAAGTGAATGTGTGTAATATATGCACTGACAGATTAATGAAGATACAGT	1392
Db	1213	GCACCCATTAAGTGAATGTGTGTAATATATGCACTGACAGATTAATGAAGATACAGT	1272
Oy	1393	CTTGACCTGGCTTACCAATTGGCCATGAGCTGTGACACAACTTTGGCATATTCATGAT	1452
Db	1273	CTTGACCTGGCTTACCAATTGGCCATGAGCTGTGACACAACTTTGGCATATTCATGAT	1332
Oy	1453	GGAGAAGGGAACATGTGTAAAAAGTCCGAGGGCAACATCATGTCCCTTACATTGGCAGGA	1512
Db	1333	GGAGAAGGGAACATGTGTAAAAAGTCCGAGGGCAACATCATGTCCCTTACATTGGCAGGA	1392
Oy	1513	CGCAATGGAAGCTCTCTCTGTGTAACCTGACCGCCAGATATTCACAAATTTCTAAGC	1572
Db	1393	CGCAATGGAAGCTCTCTCTGTGTAACCTGACCGCCAGATATTCACAAATTTCTAAGC	1452
Oy	1573	ACCGCTCAAGCTATCTGCCTTGTCTGATCAGCCAAAGCCTGTGAAGAAATACAAATATCTT	1632
Db	1453	ACCGCTCAAGCTATCTGCCTTGTCTGATCAGCCAAAGCCTGTGAAGAAATACAAATATCTT	1512

QY 1633 GAGAAATTGCCAGAGAAATTATATGATGCAAAACAACAGTGCAGTGGCAGTTCCGAGAG 1692  
DB 1513 GAAAAATTGCAAGAGAAATTATATGATGCAAAACAACAGTGCAGTGGCAGTTCCGAGAG 1572  
QY 1693 AAGCCAAAGCTGTGCATGTGTGACTTTAAAGAACATCTGTAAAGCCCTGTGTCCAT 1752  
DB 1573 AAGCCAAAGCTGTGCATGTGTGACTTTAAAGAACATCTGTAAAGCCCTGTGTCCAT 1632  
QY 1753 CGTATTGGAAGAAATGTGAGACTAAATTTATGCCAGACAGAGGCAAAATTTGTGG 1812  
DB 1633 CGTATTGGAAGAAATGTGAGACTAAATTTATGCCAGACAGAGGCAAAATTTGTGG 1692  
QY 1813 CATGACATGTGTGTGCGGGGAGAGACAGTGTGTAATATGTATGTAAGGCCCAAGCCC 1872  
DB 1693 CATGACATGTGTGTGCGGGGAGAGACAGTGTGTAATATGTATGTAAGGCCCAAGCCC 1752  
QY 1873 ACCCATGAGCACTGTGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1932  
DB 1753 ACCCATGAGCACTGTGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1812  
QY 1933 GGAGTATCTCATAGAGATGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1992  
DB 1813 GGAGTATCTCATAGAGATGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1872  
QY 1993 TGTGAGAGGCTCCCACTGCACTGTGAGCTGTGAGACCAACCCCAAGCCATGCGATGAGAGAGTT 2052  
DB 1873 TGTGAGAGGCTCCCACTGCACTGTGAGCTGTGAGACCAACCCCAAGCCATGCGATGAGAGAGTT 1932  
QY 2053 GTTGAATTCCTGCTGTGCTGAGTGTGCGAGCAACAAGAGAGAGAGAGAGAGAGAGAG 2112  
DB 1933 GTTGAATTCCTGCTGTGCTGAGTGTGCGAGCAACAAGAGAGAGAGAGAGAGAGAGAG 1992  
QY 2113 TACAAAGTGAAGCTTTACACTCAAGTGAAGAGATCAAGACTTATGCAACTTACTGTATC 2172  
DB 1993 TACAAAGTGAAGCTTTACACTCAAGTGAAGAGATCAAGACTTATGCAACTTACTGTATC 2052  
QY 2173 GCAGAGAGATTTGATTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 2232  
DB 2053 GCAGAGAGATTTGATTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 2112  
QY 2233 TCGAGAGATGAGCGTATGATTTGTATGATGAGATGATGAGAGATTTGATGATGATGAT 2292  
DB 2113 TCGAGAGATGAGCGTATGATTTGTATGATGAGATGATGAGAGATTTGATGATGATGAT 2172  
QY 2293 GTTCTTGAATCTGATGCTGTGTAAGACGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2352  
DB 2173 GTTCTTGAATCTGATGCTGTGTAAGACGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2232  
QY 2353 TGCAGAGATTCAGAGGGGTCTTACACCAAGACCAACCAACCAAGATTTATTCACATG 2412  
DB 2233 TGCAGAGATTCAGAGGGGTCTTACACCAAGACCAACCAACCAAGATTTATTCACATG 2292  
QY 2413 GTTCAACATTCCTTCTGAGACCCGAGATATCCGATCTATGAATGAACCTTCTTCACTCC 2472  
DB 2293 GTTCAACATTCCTTCTGAGACCCGAGATATCCGATCTATGAATGAACCTTCTTCACTCC 2352  
QY 2473 TACATTTCTGTGTGCAATGCTCTCAGAGGATCTTGAATGAGCACTGAGACCTGTGAC 2532  
DB 2353 TACATTTCTGTGTGCAATGCTCTCAGAGGATCTTGAATGAGCACTGAGACCTGTGAC 2412  
QY 2533 TGGCCCGGCGGAGAAATTTTTCGAGCACTTTTTCGATTCAGACAGGCTCTTATATGAG 2592  
DB 2413 TGGCCCGGCGGAGAAATTTTTCGAGCACTTTTTCGATTCAGACAGGCTCTTATATGAG 2472  
QY 2593 CCCGAGAACTTATCTCTACTGAGCAACCAACGAGACACTGATTTGTGAGAGCTGTGTT 2652  
DB 2473 CCCGAGAACTTATCTCTACTGAGCAACCAACGAGACACTGATTTGTGAGAGCTGTGTT 2532  
QY 2653 CAGGAGAGAAACCCGGGT 2712  
DB 2533 CAGGAGAGAAACCCGGGT 2592  
QY 2713 CAGCCCGGCGGAGCAAGCTTATGAGGAGATGAGGCTCTGAGAGCTCTGAGTCC 2772

DB 2593 CAGCCCGGCGGAGCAAGCTTATGAGGAGATGAGGCTCTGAGAGCTCTGAGTCC 2652  
QY 2773 TCGGAGAGGGG 2783  
DB 2653 TCGGAGAGGGG 2663

RESULT 3  
US-09-930-872-5  
; Sequence 5, Application US/09930872  
; Patent No. 6448388  
; GENERAL INFORMATION:  
; APPLICANT: Fridge, Carl Johan  
; APPLICANT: Hilpun, Erin  
; TITLE OF INVENTION: No. 6448388e1 Human Proteases and Polynucleotides Encoding the San  
; FILE REFERENCE: LEX-0219-USA  
; CURRENT APPLICATION NUMBER: US/09/930,872  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 4042  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-930-872-5

Query Match 64.8%; Score 1874.6; DB 3; Length 4042;  
Best Local Similarity 84.4%; Pred. No. 0; Mismatches 179; Indels 245; Gaps 6;  
Matches 2887; Conservative 0;

QY 202 GCAGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 261  
DB 167 GCAGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 226  
QY 262 GGTCTCTCTCTCAACCGCGGAGCGGCGGCTGTGATGTAAGAGGCGGAGCATGATGAA 321  
DB 227 GGTCTCTCTCTCAACCGCGGAGCGGCGGCTGTGATGTAAGAGGCGGCGGCGGCGGCGG 273  
QY 322 GGTGAAACATGCTTCTCAGCAAACTAAACAAGAGAACAAACCAACCTGATGTT 381  
DB 274 ----- 273  
QY 382 CTCACTCAATATGACCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 441  
DB 274 -----AATATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 326  
QY 442 CATGAATATGACATCAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 501  
DB 327 CATGAATATGACATCAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 386  
QY 502 CTTCACCTTGGCTGAAGAGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 561  
DB 387 CTTCACCTTGGCTGAAGAGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 446  
QY 562 AGCCTAGTGTCTCTGCTTATTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 621  
DB 447 AGCCTAGTGTCTCTGCTTATTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 506  
QY 622 CAGACTTAAACCGGAG 681  
DB 507 CAGACTTAAACCGGAG 566  
QY 682 TCGCAGATGAG 741  
DB 567 TCTCTA-----GTGGCTTTTCAACCTGCAAGAGCTTTGCA 602  
QY 742 AGTCAGAAATGTCCCGGAG 801  
DB 603 GGCATGATGAG 662

OY	802	AGCAACGATTCAGAGGGCGGCACTACAAGTGG--AACTTCACCTCAAGTAAGAAGCC	859
Db	663	TGGAATCTGGGAGAGCTGCCCAAGGCAAGCTCGCATCCACGTACTGTACAAGAGATCC	722
OY	860	ACTTATGCAAACTCTACTGTATCGCAGAAGATTGATTTCTCTCTTTCTTGTCAATA	919
Db	723	ACAGAGCCCACTGCTCTCTGGGCGAGTAGAGTCTCTGTGACTC-----AAGG	770
OY	920	AACTCAAAAGATGGGACTCCATGCTCGAGAGATAGCCGTAAATGTTTGTATAGATGGGATAT	979
Db	771	ACATGGGAGCTGGCACAATCAACCCCTGCACAGCAGCATCTTCGGCTGGGACTGGCACA	830
OY	980	GTGAGCTCAGTGTGGTGTCCACATCTGC-GCACATGCCCCAGGCTCCCAAGAAAGACTC	1038
Db	831	AAGCAGCATTTCTGTGGAAAGACGCAAGAAATACATGCCCCAGGCTCCCAAGAAAGACTC	890
OY	1039	TTCACTCTTGGCAGATGAGTATATAGCTTGCTTACGGCATTAAGCGCTCTTCTGAGGTCC	1098
Db	891	TTCACTCTTGGCAGATGAGTATATAGCTTGCTTACGGCATTAAGCGCTCTTCTGAGGTCC	950
OY	1099	CATAGAAATGAAGAACTGAACTGTGAGACCTTGTGTGTGTGACAAAAAGATGATGCA	1158
Db	951	CATAGAAATGAAGAACTGAACTGTGAGACCTTGTGTGTGTGACAAAAAGATGATGCA	1010
OY	1159	AACTATGGCATGAAATATATCAACCTTACTGTGTCTCAGATATCTCAACATGTATCTGCT	1218
Db	1011	AACTATGGCATGAAATATATCAACCTTACTGTGTCTCAGATATCTCAACATGTATCTGCT	1070
OY	1219	TTATTCAAGA------	1229
Db	1071	TTATTCAAGAATGAAACAATAGAGAAACATCAACATTGCAATTGATGTTGATCTT	1130
OY	1230	-----	1229
Db	1131	CTAGAAGATGAACAGCCAGGACTGTGTATATGTCAACAGGACACCACTTAAATGATAC	1190
OY	1230	-----TGATTTAGTGGGAAAGATGGGACTCGTCATGACCAAGCATC	1272
Db	1191	TTCTGCGACGTGAGCAAGCTGTGATTTAGTGGGAAAGATGGGACTCGTCATGACCAAGCATC	1250
OY	1273	TTACTGACTGTGGATATATATGTTCCGTGAAAGATGAGCCCTGTGACACTTTGGGATTT	1310
Db	1251	TTACTGACTGTGGATATATATGTTCCGTGAAAGATGAGCCCTGTGACACTTTGGGATTT	1310
OY	1333	GCACCCATAGTGAATGTATGTAAATCGCAGCTCAGAGATTAAGAATACAGGT	1392
Db	1311	GCACCCATAGTGAATGTATGTAAATCGCAGCTCAGAGATTAAGAATACAGGT	1370
OY	1393	CTTGGACTGGCCCTTCAACATTGCCATGAGTCTGTGACCAACTTTGGCATGATCATGAT	1452
Db	1371	CTTGGACTGGCCCTTCAACATTGCCATGAGTCTGTGACCAACTTTGGCATGATCATGAT	1430
OY	1453	GGAGAAAGGAAACATGTGTAAAAAGTCCGAGGGCAACATCATGTCCCTTACATTGGCAGA	1512
Db	1431	GGAGAAAGGAAACATGTGTAAAAAGTCCGAGGGCAACATCATGTCCCTTACATTGGCAGA	1490
OY	1513	CGCAATGAGTCTTCTCTGTGCAACCTGCAGCGCAGATATCTACAAATTTCTAAGC	1572
Db	1491	CGCAATGAGTCTTCTCTGTGCAACCTGCAGCGCAGATATCTACAAATTTCTAAGC	1550
OY	1573	ACCGCTCAAGCTATCTGCTTGTCTGATCAGCCAAAGCCTGTGAAGAAATACAGATATCTT	1632
Db	1551	ACCGCTCAAGCTATCTGCTTGTCTGATCAGCCAAAGCCTGTGAAGAAATACAGATATCTT	1610
OY	1633	GAGAAATTGCCAGAGGAATTATATGATCCAAACACACAGTCCACAGTGCACATTCGGAGAG	1692
Db	1611	GAGAAATTGCCAGAGGAATTATATGATCCAAACACACAGTCCACAGTGCACATTCGGAGAG	1670
OY	1693	AAAGCGAAGCTCTGATCTGTGACTTTTAAAAAGACATCTGTAAAGCCCTGTGGTGCAT	1752
Db	1671	AAAGCGAAGCTCTGATCTGTGACTTTTAAAAAGACATCTGTAAAGCCCTGTGGTGCAT	1730
OY	1753	CGTATTTGAGAAATGTGTAGACTTAAATTTATGCCAGCAGCAGAAAGCAATTTGTGGG	1812

Db	1731	CGATTGGAGGAAATGTGAGACTTAAATTTATGCCAGCACGAAAGCCAAATTTGTGGG	1790
OY	1813	CATGACATGTGGTGGCCGGGAGAGACAGTGTGTGAAATATGTGATGATGAGGCCCCAAAGCCC	1872
Db	1791	CATGACATGTGGTGGCCGGGAGAGACAGTGTGTGAAATATGTGATGATGAGGCCCCAAAGCCC	1850
OY	1873	ACCATTGGCCACTGGTCCGACTGTGCTTCTTGGTCCCATGCTCCAGAACCTGCGGAGGG	1932
Db	1851	ACCATTGGCCACTGGTCCGACTGTGCTTCTTGGTCCCATGCTCCAGAACCTGCGGAGGG	1910
OY	1993	GGAGATCTCATAGGAGTGGCTCTGACCAACCCCAAGCCATCGATGAGAGGAAAGTTTC	1992
Db	1911	GGAGATCTCATAGGAGTGGCTCTGACCAACCCCAAGCCATCGATGAGAGGAAAGTTTC	1970
OY	1993	TGTGAGGGCTCCACTCGCACTCTGAGCTCTGCAACAGTCAGAAAATGTCCCGGAGCAGT	2052
Db	1971	TGTGAGGGCTCCACTCGCACTCTGAGGCTCTGCAACAGTCAGAAAATGTCCCGGAGCAGT	2030
OY	2053	GTTGACTTCCGCTGCTCTCAGTGTGTCGCGACCAACAGGACACGATTCTGAGAGGGCGGCAC	2112
Db	2031	GTTGACTTCCGCTGCTCTCAGTGTGTCGCGACCAACAGGACACGATTCTGAGAGGGCGGCAC	2090
OY	2113	TACAAGTGGAAAGCCTTACACTCACTAGAGATGACGAACTTATGCAAACTCTACTGATTC	2172
Db	2091	TACAAGTGGAAAGCCTTACACTCACTAGAGATGACGAACTTATGCAAACTCTACTGATTC	2150
OY	2173	GCAGNAGGATTGATTTCTTCTTTTCTTTTGTCTCAAAATAAGTCAAAAGATGGACTCCATGC	2232
Db	2151	GCAGNAGGATTGATTTCTTCTTTTCTTTTGTCTCAAAATAAGTCAAAAGATGGACTCCATGC	2210
OY	2233	TCGGAGATAGCCGTAATGTTTGTATATGATGGGATATGTGAGAGAGTTGGAATGTGCAAT	2292
Db	2211	TCGGAGATAGCCGTAATGTTTGTATATGATGGGATATGTGAGAGAGTTGGAATGTGCAAT	2270
OY	2293	GTCCTTGGATCTGATGCTGTGTAACAAGTCTGTGGGGGTGTGTAACGGGAATTAAGTCAAGC	2352
Db	2271	GTCCTTGGATCTGATGCTGTGTAACAAGTCTGTGGGGGTGTGTAACGGGAATTAAGTCAAGC	2330
OY	2353	TGCAAGATTCACAGGGGTCTCTACACCAAGCACCAACACCAACAGATTAATTCACATG	2412
Db	2331	TGCAAGATTCACAGGGGTCTCTACACCAAGCACCAACACCAACAGATTAATTCACATG	2390
OY	2413	GTCACCAATTCCTTCTGAGCCCGGAGATTCGCGACTATGAAATGAAAGTCTCTACCTCC	2472
Db	2391	GTCACCAATTCCTTCTGAGCCCGGAGATTCGCGACTATGAAATGAAAGTCTCTACCTCC	2450
OY	2473	TACAAATTCGTGGCGAATGACCCTCGAAGGATCTACCTGAAATGGGACCTGGAACCGGAGAC	2532
Db	2451	TACAAATTCGTGGCGAATGACCCTCGAAGGATCTACCTGAAATGGGACCTGGAACCGGAGAC	2510
OY	2533	TGGCCCGGCGGGTCAAAATTTTCGGGCACTACTTTGCACTACAGACGGTCTCTAATATGAG	2592
Db	2511	TGGCCCGGCGGGTCAAAATTTTCGGGCACTACTTTGCACTACAGACGGTCTCTAATATGAG	2570
OY	2593	CCCGAGAACTTAAATGCTTACCTGACCAACCAACGAGACACTGATTTGTGAGAGCTGCTGTTT	2652
Db	2571	CCCGAGAACTTAAATGCTTACCTGACCAACCAACGAGACACTGATTTGTGAGAGCTGCTGTTT	2630
OY	2653	CAGGGAAGGAAACCGGGGTGTGGCTCGGGAAATATCTCATGAGCTCGGCTGGGGACCGGAAG	2712
Db	2631	CAGGGAAGGAAACCGGGGTGTGGCTCGGGAAATATCTCATGAGCTCGGCTGGGGACCGGAAG	2690
OY	2713	CAGCCCTTCGCCACGCCAGCTACACTTGGGCGCATGTGCGCTCTGAGAGTCTCCGATGCC	2772
Db	2691	CAGCCCTTCGCCACGCCAGCTACACTTGGGCGCATGTGCGCTCTGAGAGTCTCCGATGCC	2750
OY	2773	TGCGGAGGGGG 2783	
Db	2751	TGCGGAGGGGG 2761	

## RESULT 4



QY 1873 ACCCATGCGCATGCTGCGACTGCTCTTCTTGTGCTCCCATGCTCCAGACCTCGGAGG 1932  
DB 1851 ACCCATGCGCATGCTGCGACTGCTCTTCTTGTGCTCCCATGCTCCAGACCTCGGAGG 1910  
QY 1933 GAGATATCTATAGAGATGCGCTCTGCGACCAACCCAGCATGCGATGAGGAAATTC 1992  
DB 1911 GAGATATCTATAGAGATGCGCTCTGCGACCAACCCAGCATGCGATGAGGAAATTC 1970  
QY 1993 TGTGAGGAGCTCCACTGCGCATCTGAAGCTCGCAAGCTGCAAAATGTCCCGGAGCAGT 2052  
DB 1971 TGTGAGGAGCTCCACTGCGCATCTGAAGCTCGCAAGCTGCAAAATGTCCCGGAGCAGT 2030  
QY 2053 GTTGACTTCCGCTGCTGCTGAGTGTGCGAGCACAACAGCAGATTCAGAGGCGGAC 2112  
DB 2031 GTTGACTTCCGCTGCTGCTGAGTGTGCGAGCACAACAGCAGATTCAGAGGCGGAC 2090  
QY 2113 TACAGATGGAAGCTTACCTACCTAAGTAAGATCAGAGCTTATGCAACTCTATCTATC 2172  
DB 2091 TACAGATGGAAGCTTACCTACCTAAGTAAGATCAGAGCTTATGCAACTCTATCTATC 2150  
QY 2173 GCAGAGGATTTATTTCTTCTTCTTGTCAAAATGAAGTGGAGCTCCATGC 2232  
DB 2151 GCAGAGGATTTATTTCTTCTTGTCAAAATGAAGTGGAGCTCCATGC 2210  
QY 2233 TCGAGAGATGAGCGTATGTTGTATAGATGGAATGTGAGAGATTTGATGCAAT 2292  
DB 2211 TCGAGAGATGAGCGTATGTTGTATAGATGGAATGTGAGAGATTTGATGCAAT 2270  
QY 2293 GTCTCTGATCTGATGCTGTGTAAGACGTCTGTGGGTGTGTAACGGGAATTACTACGC 2352  
DB 2271 GTCTCTGATCTGATGCTGTGTAAGACGTCTGTGGGTGTGTAACGGGAATTACTACGC 2330  
QY 2353 TGCAGATTTACAGGGGTCTCTACCAACAGCACAACCAACAGATTTATCAATG 2412  
DB 2331 TGCAGATTTACAGGGGTCTCTACCAACAGCACAACCAACAGATTTATCAATG 2390  
QY 2413 GTACACATTCCTTCTGAGCGCGGAGTATCGCATCTATGAAATGAACGTCTACCTCC 2472  
DB 2391 GTACACATTCCTTCTGAGCGCGGAGTATCGCATCTATGAAATGAACGTCTACCTCC 2450  
QY 2473 TACATTTCTGTGCGCAATGCTCTCAAGAGTACTACTGAATGGGCACTGGACCGTGGAC 2532  
DB 2451 TACATTTCTGTGCGCAATGCTCTCAAGAGTACTACTGAATGGGCACTGGACCGTGGAC 2510  
QY 2533 TGGCCCGGCGGTAATAATTTTGGGCACTTGTGCACTACAGAGGTCTTAATGAG 2592  
DB 2511 TGGCCCGGCGGTAATAATTTTGGGCACTTGTGCACTACAGAGGTCTTAATGAG 2570  
QY 2593 CCCGAAATTTAATGCTACTGAGCAACCAAGACACTGATTGTGAGCTGTGTT 2652  
DB 2571 CCCGAAATTTAATGCTACTGAGCAACCAAGACACTGATTGTGAGCTGTGTT 2630  
QY 2653 CAGGAAAGGAACCCGGGTTTCTTGGAAATCTCCATGCTGTGGGACCGAAG 2712  
DB 2631 CAGGAAAGGAACCCGGGTTTCTTGGAAATCTCCATGCTGTGGGACCGAAG 2690  
QY 2713 CAGCCCTGCGGACGCGCACTACCTTGGGCAATGCTGGCTCTAGAGCTCCGTTCC 2772  
DB 2691 CAGCCCTGCGGACGCGCACTACCTTGGGCAATGCTGGCTCTAGAGCTCCGTTCC 2750  
QY 2773 TCGGAGGAGG 2783  
DB 2751 TCGGAGGAGG 2761

RESULT 5  
US-09-930-872-1  
; Sequence 1, Application US/09930872  
; Patent No. 6448388

; GENERAL INFORMATION:  
; APPLICANT: Fridde, Carl Johan  
; APPLICANT: Hilbun, Erin

; TITLE OF INVENTION: No. 6448388e1 Human Proteases and Polynucleotides Encoding the San  
; FILE REFERENCE: LEX-0219-USA  
; CURRENT APPLICATION NUMBER: US/09/930,872  
; CURRENT FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: US 60/225,852  
; PRIOR FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1476  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-930-872-1

Query Match 22.9%; Score 663; DB 3; Length 1476;  
Best Local Similarity 71.5%; Pred. No. 2,5e-183;  
Matches 1079; Conservative 0; Mismatches 185; Indels 245; Gaps 6;

QY 202 GCAGGACCTGCGTGGCCATGAGGACCGCAGCGGAGCGCTGGAGCCCGAGCGTCCC 261  
DB 69 GCAGGACCTGCGTGGCCATGAGGACCGCAGCGGAGCGCTGGAGCCCGAGCGTCCC 128  
QY 262 GCGTCTCTCCACCGCGGAGCGCGGCTGATGAGAAAGGCGGCAATGATGA 321  
DB 129 GCGTCTCTCCACCGCGGAGCGCGGCTGATGAGAAAGGCGG----- 175  
QY 322 GCTGAAACCATGTTCTCAGCAACTAAACAGAAAGAAACCAACATGATGTT 381  
DB 176 ----- 175  
QY 382 CTCACCTAATATGACCTGCTCTGCTTACAGAGTTGACACAGGCGATTAAGTCTC 441  
DB 176 -----AATATGACCTGCTCTGCTTACAGAGTTGACACAGGCGATTAAGTCTC 228  
QY 442 CATGAATATATGACCATATAGCGCGGAGAAAGAGAGCGTCCGATGATGAGTCT 501  
DB 229 CATGAATATATGACCATATAGCGCGGAGAAAGAGAGCGTCCGATGATGAGTCT 288  
QY 502 CTTACACTTCGCTGAAAGGCCCAAGGACGACTTCCATGATCTGAGACTTCCAGC 561  
DB 289 CTTACACTTCGCTGAAAGGCCCAAGGACGACTTCCATGATCTGAGACTTCCAGC 348  
QY 562 AGCTAGTGGCTCTGCTTATTTGACAGGTTGGAAGACAGGACTAAAGTCTGTC 621  
DB 349 AGCTAGTGGCTCTGCTTATTTGACAGGTTGGAAGACAGGACTAAAGTCTGTC 408  
QY 622 CAGACTTTACCGCAGAGGACTTCTTCTATCAAGGCTCTTTGGGATCAACAGAAAC 681  
DB 409 CAGACTTTACCGCAGAGGACTTCTTCTATCAAGGCTCTTTGGGATCAACAGAAAC 468  
QY 682 TGGCCATGCGATGAGAGGAAGTTCTGTAGGGGCTCCACTCGCACTGTAAGCTTGCAC 741  
DB 469 TGGCCATGAG-----CCCTTCAACCTGCGCAAGGCTTGTCA 504  
QY 742 AGTCAGAAATGTCCTCCGAGCAGGTGTGACTTCCGCTGCTCAGTGTCCGAGCAAC 801  
DB 505 GGCATGATACGAACAAGAGGAGATTACTTCTTAAGGCACTTCTTCAACCTCTCA 564  
QY 802 AGCAGAGATTTAGAGGCGGCACTACAGTGG--AAGCTTACATCAATGAAGCG 859  
DB 565 TGGAACTCGGAGAGCTCCCAAGGCACTCGCCATCCAGATCTGTACAGAGATCC 624  
QY 860 ACTTATGCAACCTTACCTGATTCGAGAGGATTTGATTTCTTCTTTGTCAATA 919  
DB 625 ACAGAGCCCAATGCTCTTGGGCTCAGTAGGTCTGTGATCTC-----AAGG 672  
QY 920 AAGTCAAGATGAGACTCCATGCTCGAGAGATAGCGTATGTTGTATAGATGAGATAT 979  
DB 673 ACATGGAAGCTGGCATATCAACCCCTGCAAGAGGACTTCCGCTGGAGCTGCACAA 732  
QY 980 GTGAGCTAGTGTGTGTCAATCTGCGC-AATGCCCCAGCTTCCAGAGAAAGCTTC 1038  
DB 733 AAGCAGCATTTCTGTGAAGAGCAAGAAATACATGCCCCAGCTTCCAGAGAAAGCTTC 792

QY 1039 TTCAATCTTGCCAGAAAGAGTATTAAAGTCCTTGCTTAAGGCGCATTAAGCGCTCTCTCTGAAGGTCC 1098

Dd 793 TTCATCTTTGCCAAGAAGATATAAGTCTTGCTTAAAGGCGATTAAGCGCTCTCTCTGAAGGTCC 852

OY 1099 CATAGAAATGAAAGACGTAAACGTGGAGACTTGGTGGTGGTGCACAAAAAAGATGATGCAA 1158

Dd 853 CATAGAAATGAAAGACGTAAACGTGGAGACTTGGTGGTGGTGCACAAAAAAGATGATGCAA 912

OY 1159 AACATGGCCATGAAAAATATACACACCTAGCGTCTCAGATAGCTCAACATGTAATCTGCT 1218

Dd 913 AACATGGCCATGAAAAATATACACACCTAGCGTCTCAGATAGCTCAACATGTAATCTGCT 972

OY 1219 TTAATCAAGA----- 1229

Dd 973 TTAATCAAGAATGGAACAATAGAGAAAAATCAACATTTGCAATTGTAAGTCTGATTTCTT 1032

OY 1230 ----- 1229

Dd 1093 CTAGAAAGATGAACAGCCAGAGACTGGTGTATTAAGTACACAGAGAACACACCTTAAGTAGC 1092

OY 1230 -----TGAATTGATGGGGAAGATGGGACTTCGTATGACCAAGCCATC 1272

Dd 1093 TTCTGCCAGTGGCACTCTGGAATTGATGGGGAAGATGGGACTTCGTATGACCAAGCCATC 1152

OY 1273 TTAATGACTGGTCTGGATATATNGTTCCGGAAGAAATGAGCCCTGTCACATTTGGGATTT 1332

Dd 1153 TTAATGACTGGTCTGGATATATNGTTCCGGAAGAAATGAGCCCTGTCACATTTGGGATTT 1212

OY 1333 GCACCCTAAGTGAATGTGATGTAATATATCGACGTGCAAGATTAATGAAATACAGT 1392

Dd 1213 GCACCCTAAGTGAATGTGATGTAATATATCGACGTGCAAGATTAATGAAATACAGT 1272

OY 1393 CTTGGAATCTGGCTTCAACATTTGCCATATGATCTGGAACAACAATTTGGCATATTCATGAT 1452

Dd 1273 CTTGGAATCTGGCTTCAACATTTGCCATATGATCTGGAACAACAATTTGGCATATTCATGAT 1332

OY 1453 GGAAGAAAGGAAACATGTGTAAAGAGTCGAGGGCAAAATCATGTCCCCTACATTTGGCAGGA 1512

Dd 1333 GGAAGAAAGGAAACATGTGTAAAGAGTCGAGGGCAAAATCATGTCCCCTACATTTGGCAGGA 1392

OY 1513 CGCAATGAGAGTCTTCTCCTGTGTCACCTGACGCGCCAGATCTTACACAAATTTCTAAGC 1572

Dd 1393 CGCAATGAGAGTCTTCTCCTGTGTCACCTGACGCGCCAGATCTTACACAAATTTCTAAGC 1452

OY 1573 ACCGCTCAA 1581

Dd 1453 TCAGTGAAA 1461

RESULT 6  
US-10-217-774-1  
; Sequence 1, Application US/10217774  
; Patent No. 6734007  
; GENERAL INFORMATION:  
; APPLICANT: Fiddler, Carl Johan  
; APPLICANT: Hilburn, Erin  
; TITLE OF INVENTION: No. 6734007el Human Proteases and Polynucleotides Encoding the  
; TITLE OF INVENTION: Same  
; FILE REFERENCE: LEX-0219-USA  
; CURRENT APPLICATION NUMBER: US/10/217, 774  
; CURRENT FILING DATE: 2002-08-12  
; PRIOR APPLICATION NUMBER: US/09/930, 872  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: US 60/225, 852  
; PRIOR FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1476  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-217-774-1

Query Match	22.94;	Score 663;	DB 4;	Length 1476;
Best Local Similarity	71.5%;	Pred. No. 2.5e-183;		
Matches 1079;	Conservative 0;	Mismatches 185;	Indels 245;	Gaps 6;
QY	202	GCAGGACCTTCGCGGCATGGGAGCCCGCAGCGGACGCGCTGTGGAGACCCGAGCGTCCC	261	
Db	69	GCAGGACCTTCGCGGCATGGGAGCCCGCAGCGGACGCGCTGTGGAGACCCGAGCGTCCC	128	
QY	262	GCCTCTCTCTCACCCGCGAGCGGCGCGGCTGTGATGGAAAAAGGCGGAGCATGATGAA	321	
Db	129	GCCTCTCTCTCACCCGCGAGCGGCGCGGCTGTGATGGAAAAAGGCGGCGGCGGCGG	175	
QY	322	GCTGGAAACCATCGTTCTCAGCAAACTTAACAAGAAACAGAAAACAAACACTGCATGTT	381	
Db	176	-----	175	
QY	382	CTCACTCAATATGACCTGGTCTCTGCTTACGAGGTTGACCAAGGCGGATTAAGTGTCC	441	
Db	176	-----AATATGACCTGGTCTCTGCTTACGAGGTTGACCAAGGCGGATTAAGTGTCC	228	
QY	442	CATGAATATCAAGCAACATCAGCGCGGAGAAAGACAGTGGCGGTCTCGAGTTGAGTCT	501	
Db	229	CATGAATATCAAGCAACATCAGCGCGGAGAAAGACAGTGGCGGTCTCGAGTTGAGTCT	288	
QY	502	CTTCACTCTTCGCGCTGAAAGGCGCCGAGCAGCACTTCCACATGATCTTGAGACTTCCAGC	561	
Db	289	CTTCACTCTTCGCGCTGAAAGGCGCTCCAGGACGACCTTCCACGATGATCTTGAGACTTCCAGC	348	
QY	562	AGCTTATGCTGCTCTCGCTTTATTTGTGACAGCTTTGGGAAAGACAGGACCTTAAGTCTGTG	621	
Db	349	AGCTTATGCTGCTCTCGCTTTATTTGTGACAGCTTTGGGAAAGACAGGACCTTAAGTCTGTG	408	
QY	622	CAGACTTTACCGCGCAGAGGACTTGTGTTTCATCAAGGCTCTTTCGATCCACAGAAAC	681	
Db	409	CAGACTTTACCGCGCAGAGGACTTGTGTTTCATCAAGGCTCTTTCGATCCACAGAAAC	468	
QY	682	TCGCGCATCGATGAGAGGAAATTCTGTGAGGGCTCCACTGCACTTGAAAGCTGTGCAAC	741	
Db	469	TCCTCAGTGG-----CCCTTTCACCTGCGCAAGGCTGTGCA	504	
QY	742	AGTCAGAAATGTCCCGCGGACAGTGTGACTTCCGTGTCTGTCAGTGTCCGAGACCAAC	801	
Db	505	GGCATGTATACGAACAGAAAGGACGATTAATCTCTTAAGGCCACTTCCACACTCTGCA	564	
QY	802	AGCAGACGATTCAGAGGCGCGCACTACAAGTGG--AAAGCTTACACTCAAGTAGAACCG	859	
Db	565	TGGAATCTCGGCAAGGCTCGCCCAAGGACGCTCGCATCTCCACGTAAGTGAACAAAGATCC	624	
QY	860	ACTTATGCAAACTTACTGTATGTGCGAAGAGATTGTAATTTCTTTTCTTTTGTTCAAATA	919	
Db	625	ACAGAGCCCATGTCTCTGGGGCGAGTAGAGGTCTGTGTGACCTC-----AAGG	672	
QY	920	AAGTCAAAGATGGGACTTCATGTCTCGAGAGGTAGCCGTAATGTTGTATAGAGGATAT	979	
Db	673	ACATGGAGAGCTGGGACATCAACCCCTGCAAGCAGCAACTTGGCTGTGGAGCTGCCACAA	732	
QY	980	GTCAGCTCAGTGTGTGTCCACATCTGCGC-ACATGCCCCAGCCTCCCAAGGAAGACTC	1038	
Db	733	AAGCAGCATTTCTGTGGAAACCGCAAGAAATATCAATGCCCCAGCCTCCCAAGGAAGACTC	792	
QY	1039	TTTATCTTGGCAGATGATATAGTCTTGTCTTACCGGATTAAGGCTCTCTTGTAGGTC	1098	
Db	793	TTTATCTTGGCAGATGATATAGTCTTGTCTTACCGGATTAAGGCTCTCTTGTAGGTC	852	
QY	1099	CATGAATATGAAACATGAACTGAGACCTTGTGTGTGTCGACAAAGAAAGATGATGAA	1158	
Db	853	CATGAATATGAAACATGAACTGAGACCTTGTGTGTGTCGACAAAGAAAGATGATGAA	912	
QY	1159	AACCATGGCCATGAAATATCAACACTTACGTGTCTCAGATCTCAACATGATATCTGCT	1218	
Db	913	AACCATGGCCATGAAATATCAACACTTACGTGTCTCAGATCTCAACATGATATCTGCT	972	



QY 1219 TTATTCAMAG----- 1229  
| | | | |  
Db 973 TTATTCAMAGATGGAACAATATAGAGGAAACATCAATGCAATTTAGGTGTGATTTCTT 1032  
| | | | |  
QY 1230 ----- 1229  
| | | | |  
Db 1033 CTGAAAGATGAGACAGCCAGGACTGTGTATTAATGTCACCAAGCAGACCACTTAAAGTAGC 1092  
| | | | |  
QY 1230 ----- 1272  
| | | | |  
Db 1093 TTCTGCCAGTGGCAGTCTGTGATTTGATGGGAAAGATGGAGCTGTCTATGACACAGCCATC 1152  
| | | | |  
QY 1273 TTACTGACTGTCTGTATATATGTTCTCTGGAAGATAGCCCTGTGACATTTTGGGATTT 1332  
| | | | |  
Db 1153 TTACTGACTGTCTGTATATATGTTCTCTGGAAGATAGCCCTGTGACATTTTGGGATTT 1212  
| | | | |  
QY 1333 GCACCCCTTAAGTGAATGTGTATTAATATTCGACGCTGCAAGATTAATGAAGATACAGGT 1392  
| | | | |  
Db 1213 GCACCCCTTAAGTGAATGTGTATTAATATTCGACGCTGCAAGATTAATGAAGATACAGGT 1272  
| | | | |  
QY 1393 CTGGAAGTGGCTTCAACATTTGCCATGAGCTGTGACACAACTTTGGCATATTCATGAT 1452  
| | | | |  
Db 1273 CTGGAAGTGGCTTCAACATTTGCCATGAGCTGTGACACAACTTTGGCATATTCATGAT 1332  
| | | | |  
QY 1453 GGAGAAAGGAAACATGTGTAAAAAGTCCGAGGGCAACATCATGTCCCTACATTTGGCAGGA 1512  
| | | | |  
Db 1333 GGAGAAAGGAAACATGTGTAAAAAGTCCGAGGGCAACATCATGTCCCTACATTTGGCAGGA 1392  
| | | | |  
QY 1513 CGCAATGAGTCTTCTCTGTGTCACTCTGCAAGCCGCAATATCTACACAAATTTCTAAGC 1572  
| | | | |  
Db 1393 CGCAATGAGTCTTCTCTGTGTCACTCTGCAAGCCGCAATATCTACACAAATTTCTAAGC 1452  
| | | | |  
QY 1573 ACCGCTCAA 1581  
| | | | |  
Db 1453 TCAGTGAAA 1461  
| | | | |

RESULT 7  
US-09-963-791-23  
; Sequence 23, Application US/09963791  
; Patent No. 6649399  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Friedlich, Glenn  
; APPLICANT: Scoville, John  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sande, Arthur T.  
; TITLE OF INVENTION: No. 6649399el Human Proteases and Polynucleotides Encoding the Sa  
; FILE REFERENCE: LEX-0105-USA  
; CURRENT APPLICATION NUMBER: US/09/963,791  
; CURRENT FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: US 60/169,769  
; PRIOR FILING DATE: 1999-12-09  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 2274  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-963-791-23

Query Match 7.8k; Score 227; DB 4; Length 2274;  
Best Local Similarity 50.1k; Pred. No. 1.6e-55;  
Matches 721; Conservative 0; Mismatches 685; Indels 33; Gaps 5;  
QY 1253 CTGCTGATGACCAAGCCATCTTAATGACTGTCTGATATATGTTCTCTGGAAGATAGC 1312  
| | | | |  
Db 590 CCCACACAGATATGACAGTCTTATTTACTAGATATGATATCTGCACTTAAAAATAAGC 649  
| | | | |  
QY 1313 CCTGTGACACTTTGGGATTTGACCACTAAGTGAATGTGTAGTAATATTCGACGCTGCA 1372  
| | | | |  
Db 650 CCTGTGAACTGTGGGCTTGGCTTGTGTGCTGGAATGTGTAGCTTGAAGAGGCTGCA 709  
| | | | |

QY 1373 CGATTATGAAAGATACAGGTCCTTGAAGTCCCTTCAACCAATGGCCATGAGTGCACACA 1432  
| | | | |  
Db 710 GCATTATGAAAGATACAGGTCCTTGAAGTCCCTTCAACCAATGGCCATGAGTGCACACA 769  
| | | | |  
QY 1433 ACTTTGGCATGATTCATGATGGAAGGAAACATGTGTAAA-----ACTCCGAGG 1483  
| | | | |  
Db 770 ATTTGTGTATGAACCATGATGGAATTTGGAATTTCTTGGGAGCAAGAGTCAATGAAGCAG 829  
| | | | |  
QY 1484 GCACATCATGTCCCTTACATTTGGCAGACGCAATGAGATCTTCTCTGCTACCCCTGCA 1543  
| | | | |  
Db 830 CAAACTTATGAGAGCTCACTTATCTGCAATACCAATCTTTTCTGTGCTGCTTGA 889  
| | | | |  
QY 1544 GCCGCAATATCTACCAAAATTTCTAAGCACCGCTCAAGCTATCTGCTGTGATCAGC 1603  
| | | | |  
Db 890 GTGCAACTATCATCAGCTCTTCTAGATTTCAAGCCGTGTACTTCCCTTGAATATGAGC 949  
| | | | |  
QY 1604 CAAAGCTGTGAAGAAATCAAGATCTGAGAAATTCGCAAGAAATTAATATGATGCAA 1663  
| | | | |  
Db 950 CT---CCCAAGCGTGACTTTCTTTATCCAGCTGTGGCCCAAGGTCAAGTGTATGATGCTG 1006  
| | | | |  
QY 1664 ACACAGATGCAAGTGCAGTTCGAGAGAAAGCCAAAGCTCTGCAATGCTGACTTTAAAA 1723  
| | | | |  
Db 1007 ATGAGCAATGTGCTTCCAGATGAGCAACCTCCGCAATGTAAATATG----- 1057  
| | | | |  
QY 1724 AGGACATCTGTAAAGCCCTGTGGTGCATCTGTATGGAAGAAATGTGAGACTTAATTTA 1783  
| | | | |  
Db 1058 GGGAAATGTGTAGAGAGCTTGTGTCTCAGCAAAAGCAACCGCTGTTCACCAACAGTA 1117  
| | | | |  
QY 1784 TGGCAGACAGAAAGGACAAATTTGTGGCATGACATGTGTGCCGGGAGAGCAAGTGTG 1843  
| | | | |  
Db 1118 TTCCACAGCTGAGGGAGACATGTGTCAAACTGGGAATATGAAAAAGGTTGTTATTC 1177  
| | | | |  
QY 1844 TGAATATGTGAT-----GAAGGCCCAAGCCCAACCATGCGCATGTGTCGACT 1894  
| | | | |  
Db 1178 AGGGAATTTGTCTCTTTTGGCACTTGGCCCGCAGACATAGATGGGGCTGGGTCCCT 1237  
| | | | |  
QY 1895 GGTCTTCTGTGTCCTCCATGCTCCAGAGCTTCCGAGGGGAGATCTCATAGAGATCGCC 1954  
| | | | |  
Db 1238 GGTCTATATGGGAGAGTGCAGAGAGACTTGGGGGAGAGCGTCTCTCATCCCTTAAGAC 1297  
| | | | |  
QY 1955 TGTGACCAACCCCAAGCCATGCGATGAGAGGAATTTCTGTGAGGGCTCCATCGCACTC 2014  
| | | | |  
Db 1298 ACTGTACAGTCCAGACCTTTCAGAGGTGAAAAATTTGCTTTGGGAAAAAGAAACGGT 1357  
| | | | |  
QY 2015 TGAAGCTGTGCAACATGCAAAATGTCCCGGAGAGTGTGACTTCCGTGCTGCTCACT 2074  
| | | | |  
Db 1358 ATGCTCTCTGTAAACAGATCCATGCTTTTGGGTTCCCGAGATTTTTCAGAGAAAACAGT 1417  
| | | | |  
QY 2075 GTGCCGAGCAACACAGACGATTCAGAGGGGCGCACTAACAATGGAAGCTTTACACTC 2134  
| | | | |  
Db 1418 GTGCAAGCTTTGACATATGCTCTTTCGAGGAAAGTATTAATCTGAAACCTTAATCT- 1476  
| | | | |  
QY 2135 AAGTAGAAGATCAGACTTAATGCAACTCTACTGTATTCGCAAGGATTTGATTTCTTCT 2194  
| | | | |  
Db 1477 --GAGAGTGGGGTAAACCTGTGTGATTAACCTGTGCTGTAAGGTTTAATTTCTAAC 1534  
| | | | |  
QY 2195 TTCTCTTTCATTAATAAGTCAAAAGATGAGATCTTCATGCTTCGAGATTAAGCCGTAATGTT 2254  
| | | | |  
Db 1535 CTGAAAGTCTCTCTGGGATGATGATGAGACCCAGTGCATATGAGATTCATGAGATATCT 1594  
| | | | |  
QY 2255 GTATAGATGGAATATGAGAGAGTGTGATGTCACATGCTCTGTGATCTGATCTGTGTTG 2314  
| | | | |  
Db 1595 GCATCAATGGAATATGAGAGAGTGTGATGTCATTAATTTTGGGATCTGATGCTAGAGG 1654  
| | | | |  
QY 2315 AAGACGCTGTGTGGGATGTGTAAAGGAAATTAATCAAGCTTCGACGATTCACAGGGGTCTCT 2374  
| | | | |  
Db 1655 AAGATGATGTGAGAGTGTGAGGGGAGCGAAGACATATGATGTCATTTGAAGGGGTCTT 1714  
| | | | |  
QY 2375 ACACCAAGACACCAACCAACCAATATTAATCAATGTGTACCAATTTCTTCTGTGAGCCC 2434  
| | | | |  
Db 1715 TCATGATTTCACTGCCCAAGGGAGGCTTACATGGAAGTGTGACAGATACCAAGAGGCTCTG 1774  
| | | | |

```
QY      2435 GGAGTATCCGATCTATGAAGTGAAGTCTCTTACTCTTCAATTTCCTGCGCAATGCC 2494
Db      1775 TTCACATTGAAGTTAGAGAGTTGCCATGTCCAAAGAACTATTTGCTTAAATTCGAAG 1834
QY      2495 TCAGAAGTACTACTGAATGAGGCACTGACCGTGGACCTGCCCGCGGTCAAAATTTT 2554
Db      1835 GAGATGATTACTATTAATTAATGAGTGGCTGACTATTAAGTGGCTTAGAAATTTGATGTTG 1894
QY      2555 CCGGCACTACTTTTGCATCAGACGGTCTTAAATAGCCCGAAGAACTTAATGCTTACTG 2614
Db      1895 CTGGGACAGCTTTTCAATTACAGAGAACCACTGATGAAACAGAAATCTTGAAGCTCTAG 1954
QY      2615 GACCAACCAACGACACGATGTTGTGAGTGTCTGTTTACGAGGAAGAACCCGGGTGT 2673
Db      1955 GTCTTACTTCAGAAATCTCATGTCATGTTCTGCTTCAAGAAAGAAATTTGGGAATT 2013

RESULT 8
US-09-963-791-1
; Sequence 1, Application US/09963791
; Patent No. 6649399
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Seoville, John
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sande, Arthur T.
; TITLE OF INVENTION: No. 6649399el Human Proteases and Polynucleotides Encoding the Sa
; FILE REFERENCE: LEX-0105-USA
; CURRENT APPLICATION NUMBER: US/09/963,791
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/169,769
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2727
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-963-791-1

Query Match      7.8%; Score 227; DB 4; Length 2727;
Best Local Similarity 50.1%; Pred. No. 1.7e-55;
Matches 721; Conservative 0; Mismatches 685; Indels 33; Gaps 5;

QY      1253 CTCGTCATGACCAAGCCATCTTACTGACTGTCTGATATATGTTCTCGAAGATGAGC 1312
Db      1043 CCACACAGATATATGCAAGTTCTTATTAAGATATATCTGCACTTATTAATAAATAAGC 1102
QY      1313 CCGTGACACTTTGGGATTTGCAACCATTAAGTGAATGTGTAGTAATAATTCGACGCTGCA 1372
Db      1103 CCGTGGAACACTGGGCTTGGCTCTGTGGCTGGAATGTGTAGCTGAAAGAGCTGCA 1162
QY      1373 CGATTAAAGATATAGGCTTTGACTGGCTTCACATTCGCCATTCGCTGAGTCTTGACAA 1432
Db      1163 GCATTATATAGCATTTGGCTTGGCTTCAAGCTTTTACATTCGACATGAGATTTGGTACAA 1222
QY      1433 ACTTTGGCATGATTCATGATGAGGAAGGAACATGTGTAATA-----AGTCCGAG 1483
Db      1223 ATTTTGGTATGAACATGATGGAATTTGGAATTTCTTGTGGAGGAAGTCAATGAAGCAG 1282
QY      1484 GCAATCATATGTCCTTACATTTGGCAGAGACGCAATGAGAGTCTTTCTCTGGTCACTTGA 1543
Db      1283 CAAACTTATGGCAGCTCACTTACTGCGAATACCAATCTTTTCTCTGGTCTGCTTGA 1342
QY      1544 GCGGCGAGATCTACCAAAATTTCTAAGACCGGCTCAAGCTATCTGGCTTGTGATCAGC 1603
Db      1343 GTGAGACTTACATCAACCACTTTCTAGATTCAGGCGGTGACTTGGCTTGAATATGAGC 1402
QY      1604 CAAAGCTGTGAAGAAATCAAGTATCTGAGAAATTTGCCAGAGAAATTAATATGATGCA 1663
Db      1403 CT---CCCAAGGTGACTTTCTTTATTCACGCTGTGCCCCAGGTCAAGTGTATGATGCTG 1459
```

```
QY      1664 ACACACAGTGAAGTGGCAGTTCCGAGAGAAAGCCAAAGCTCTGCAATGCTGCACTTTAA 1723
Db      1460 ATGACCAATGTGTTTCCAGTATGAGCAACTCCCGCAATGATTAATATG----- 1510
QY      1724 AGGACATCTGTAAACCCCTGTGTGTCATCTGTAATTTGGAAGAAATGTGAGACTTAATTTA 1783
Db      1511 GGAAGATGTGTAAGAGCTGTGTGTCTCAGCAAAAGCAACCGTGTGTACCAACAGTA 1570
QY      1784 TCCAGACGACAGAAAGCAAAATTTGTGGCATGACATGTGTGTGCGGGAGAGACAGTGTG 1843
Db      1571 TTCCAGACAGCTGAGGGACACTGTGTCAAACCTGGGAATTTGAAAAAGGTGTGTATTC 1630
QY      1844 TGAATATGTGAT-----GAAAGCCCCAAGCCCAACCCATGACCACTGTGCGACT 1894
Db      1631 AGGAGATTTGTGTTCTTTTGGCATTGTGGCCCAAGACATAGATGGGGGCTGGGTCCCT 1690
QY      1895 GGTCTTTTGTGTCCTTCAGACAGTCTGTGGAGGGGAGTATCTCATAGAGTCCG 1954
Db      1691 GGTCACTATGGGAGAGTGCAGACAGGACCTGTGGGGAGGCGCTCTCATCTCAAGAC 1750
QY      1955 TCTGCACCAACCCCAAGCCATGCGATGAGAGGGAAGTTCTGTGAGGGCTCCATCCGACTC 2014
Db      1751 ACTGTGACAGTCCACACACTTTCAGAGAGGTGGAATATTTGCTTGGGAAAGAAACGCT 1810
QY      2015 TGAAGCTTGCACAGTCAGAAATGTCCCGGACAGTGTGACTTCCGTGCTGCTCACT 2074
Db      1811 ATGCTCTCTGTAAACAGATCCATCCCTTTGGTTCGAGATTTTGGAGAGAAACAGT 1870
QY      2075 GGGCGGACGACAAACGACAGATTCACAGAGGCGGCACTACAAAGTGAAGACCTTACACTC 2134
Db      1871 GTGCAGACTTTGACAAATATGCTTTCCAGAGAAATATTAATACGGAACCTCTTACT- 1929
QY      2135 AAGTAGAAGATCAGACCTTAATGCAAACTCTACTGTATGCGAAGAGATTTGATTTCTTCT 2194
Db      1930 --GAGGTGGGGTAACCTGTGTGATTAATCTGTTGGCTGTAAGTTAATATTTCTACA 1987
QY      2195 TTTCTTTGTCAAATTAAGTCAAGATGGGACTCATGCTCGAGAGATAGCGTAATGTTT 2254
Db      1988 CTGAACGTGCTCTCCGCGGTGATCGATGGGACCCAGTGCATATCGGATTCACATGATATCT 2047
QY      2255 GPATGATGGGATATGAGAGATGATGATGACAAATGTCCTTGGATCTGATGCTGTTG 2314
Db      2048 GCATATATGAGAAATGCAAGGACGTAAGCTGTGATTAATTTTGGGAATCTGATGCTAGGG 2107
QY      2315 AAGACGTCTGTGGGTGTGTATACGGGAATTAATCAAGCTGACGATTCACAGGGGTCTCT 2374
Db      2108 AAGATTAATGTGAGTCTGTGAGGGGAGCGGAAGCACATGTGATGCCATTTGAAGGTTCT 2167
QY      2375 ACACCAAGCAACCAACCAACCAAGTATATCATATGTACATCTCTCTTCTTGAAGCCC 2434
Db      2168 TCAATGATTTCACTGCCCGAGGGAGGCTACATGAAAGTGTGCAAGATACCAAGAGGCTCG 2227
QY      2435 GGAATATCCGATCTATGAATGAACGTCCTTACTCTCAATTTCTGTGGCAATGCGCC 2494
Db      2228 TTCACATTGAAGTTAGAGAGATGTCCATGTCAAAAGACTATATTTGCTTTAAATCTGAAG 2287
QY      2495 TCAGAAGTACTACTGTAATGGGCACTGACCGTGGACTGGCCCGCGGTCAAAATTTT 2554
Db      2288 GAGATGATTTACTATTAATTAATGTGTGCTGACATATTTGATGTGGCCCTAGAAATTTGATGTTG 2347
QY      2555 CCGGCACTACTTTTGCATCAGACGGTCTTATATGAGCCCGAAGAACTTAATGCTTACTG 2614
Db      2348 CTGGGACAGCTTTTCAATTAACAAGAGACCAACATGATGAACAGAAATCTTTGGAAGCTTAG 2407
QY      2615 GACCAACCAAGACATGATTTGTGAGCTGCTGTTTCAAGGAAGAAACCCGGGTGT 2673
Db      2408 GTCTTACTCAGAAATCTCATGTGATGTTCTTGTCTTCAAGAAACGAATTTGGGAATT 2466

RESULT 9
US-09-799-451-411
; Sequence 411, Application US/09799451
```

Patent No. 6783969  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Zhou, Ping  
APPLICANT: Goodrich, Ryle  
APPLICANT: Heundi, Vinod  
APPLICANT: Ren, Feiyan  
APPLICANT: Zhang, Jie  
APPLICANT: Xue, Aifeng J.  
APPLICANT: Zhao, Qiong A.  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Ma, Yunding  
APPLICANT: Yamazaki, Victoria  
APPLICANT: Chen, Rui-hong  
APPLICANT: Wang, Zhiwei  
APPLICANT: Wang, Dunrui  
APPLICANT: Yang, Yonghong  
APPLICANT: Weinman, Tom  
APPLICANT: Ghosh, Reena  
APPLICANT: Dymnac, Radoje T.  
TITLE OF INVENTION: No. 6783969el Nucleic Acids and  
FILE REFERENCE: 803  
CURRENT APPLICATION NUMBER: US/09/799,451  
CURRENT FILING DATE: 2001-03-05  
NUMBER OF SEQ ID NOS: 948  
SOFTWARE: PL\_FL\_genes Version 2.0  
SEQ ID NO 411  
LENGTH: 3571  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (260)..(3568)  
US-09-799-451-411

Query Match 7.24; Score 209.6; DB 4; Length 3571;  
Best Local Similarity 49.44; Pred. No. 2.6e-50;  
Matches 706; Conservative 0; Mismatches 689; Indels 33; Gaps 5;

1240 GGGAAAGATGGAGCTGCTGACACAGCCATCTTACTGACTGTCTGATATATGTTCC 1299  
1256 GAAAGCGTGTGTGCTAACAAGACAGAGTCTCTACACGCTATGACATCTGCATC 1315  
1300 TGGAAAGATGAGCCCTGTGACACTTTGGATTGGCAACCAATAGTGAATGTGATAA 1359  
1316 TACAAAGAACAAACCTCTGGGCACTAGGCTGGCCCGGTGGCGAAATGTGAGCCG 1375  
1360 TATCGAGCTGCAAGATTAAGAATAGATGAGTCTTGGACTGGCTTCAACCATTTGCCAT 1419  
1376 GAGAGAAAGTGCAGCGCTCAATGAGGACATTTGGCTGCGCAAGCGTTTCACTTGGCCAC 1435  
1420 GAGCTTGGACACAATTGGGATGATTCATGATGAGAGAGGAACATGT-----GT 1470  
1436 GAAATCGGGGACACATTCGGCATGACATGACGGCTGGGAAACAGCTGTGGGGCCCGT 1495  
1471 AAAAAGTCGAGGAGCAATCATGTCCCTCAATGAGGAGAGGCAATGAGTCTTCTCC 1530  
1496 GGTCAAGAACCCAGCAAGCTCAATGCTGCCCACTTACATGAAGAACCAACCAATTCGTG 1555  
1531 TGGTCAACCTGCAAGCCCGCAGATCTTACACAAATTTCTAAGCAACCGCTCAAGCTATCTGC 1590  
1556 TGGTCAATCTTGCAACCGTGACTACATCAACGAGTTTCTAAGCTCGGGCTGGGCTCTGC 1615  
1591 CTTCGATGATCAAGCAAGCTGTGAAGAAATCAAGTATCTTGAAGAAATTTGCCAGAGAA 1650  
1616 CTGAACAACCGGCC---CCCAAGACAGACTTGTGTATGACCAAGTGGACCGGGCCAA 1672  
1651 TTATATGATGACAAACACAGTGCAGTGGCAAGTTGGAGAGAGAAAGCCAGCAAGCTGTGAGT 1710  
1673 GCGTCAATGATGAGTGAAGTGGCTTTCAGATGAGATGAAATGCGCTCAAGTGTAAA 1732  
1711 CTGGAATTTAAAAAGACATCTGTAAAGCCCTGTGTGTCATGTATTTGAAGAAATGT 1770

1733 TACG-----GGAGGCTCTGAGCGAGCTGTGTGTGAGCAAGACCAACCGGTGC 1783  
1771 GAGACTAAATTTATGACAGACAGAAAGCAAAATTTGTGG-----CATTCATG 1821  
1784 ATCAACCAAGACATCCCGGCGCCAGAGGACCTGTGCGACAGCAACCATATGACAAAG 1843  
1822 TGGTCCGGGAGAGACAGTGTGTGAATAATGTGATGAAGAGCCCAAGCCCACTATGCG 1881  
1844 GGGTGGTGTCAAAAGGGCTGTGTGTCTTGGGTGGGTCGCGCAAGGGTGTGAGCGAG 1903  
1882 CACTGTGCACTGTGTCTTGTGTCCATGCTTCAAGAACCTTGGAGAGGGAGATATCT 1941  
1904 GCGTGGGGGCGTGTGACTCCATGGGGCACTGACGGCGGACTGTGGCGGGCGGTCTCC 1963  
1942 CATAGAGTGGCTCTGACCAACCCCAAGCCATTCGATGAGAGGAAATTTGTGAGGGC 2001  
1964 TCTTCTAGTGTCTACGTGACAGACCCCAAGCCAACTCGGGGCAAGTACTGTCTGGGT 2023  
2002 TCCACTGCACTCTGAAGCTCTGCAACAGTCAAGAAATGTCCCGGAGCAAGTGTGACTTC 2061  
2024 GAGAGAAAGCGGACCGGCTCTGCAACAGGATGATGTCTCCCTGCTCCAGACTTC 2083  
2062 CGTGTGCTCAAGTGTGCGGACCAACAGCAGATTCAGAGGCGGCACTTCAAGTGG 2121  
2084 AGAAGTGTGAGTGTCTGAATTTGACAGCATCTTCCGTGGGAAATTTCAAGTGG 2143  
2122 AACCTTACACTAAGTGAAGATCAGACTTATGCAAACTCACTGATTCGAGAGGA 2181  
2144 AAAACGTACCGGGAGGGGCGTGAAGGCC--TGTCTGCTCAGTCCAGTGAAGAGGC 2200  
2182 TTTGATTTCTTCTTTCTTTTGTCAATTAAGTCAAAAGATGAGACTCCATGCTCGAGAT 2241  
2201 TTCACTTCTACACAGAGAGGGGCGAGCGGTGTGAGAGGAGACCTTCCGCTCCAGAC 2260  
2242 AGCCGTAATGTTGTATATGATGATATGTGAGAGTGTGATGATGATGATGATGATGAT 2301  
2261 ACGTGTGACATTTGCGTCAAGTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2320  
2302 TCTGATGCTGTGGAAGACGCTGTGGGGTGTGTAAGGGAATTAACAGCTGCAAGAT 2361  
2321 TCCGACCTCGGAGAGACAGATGCCAGTGTGTGGCGGTGACGGCAGTGTCTGAGAGCC 2380  
2362 CACAGGGTCTCTTACACCAAGCACCACCAACCAACAGTATATGACATGTCACATT 2421  
2381 ATGAGAGGCGTCTTCAAGCCAGCTCACTCGGGGCGGGGTACAGAGATGTCTGTGATT 2440  
2442 CTTTGTGAGGCGGAGTATCCGATCTATGAATGAAGGTCCTTCACTTCAATTTCT 2481  
2441 CCCAAGGCTCGGTCAACATCTTCAATCAGAGATCTGAACCTCTCTCACTGACTTGGCC 2500  
2482 GTGCGCAATGCTCTGAGAAAGTACTACCTGAATGAGGCACTGAGACCTGTGAGTGGCCCGG 2541  
2501 CTGAAGGAGACCAAGAGTCCCTGTGTGAGAGGGCTGTGGAGACCCCGAGCCCAAC 2560  
2542 CGGTACAAATTTTGGGCACTACTTTCAGCTACAGACGGGCTCTATATGAGCCGAGAAC 2601  
2561 CGTGTGCTCTAGCTGTGAGACCACTTTCACTGCAAGAGGCGCAACAGAGTCTCAGAGC 2620  
2602 TTAATGCTAATGAGCAACCAACAGAGACATGATTTGTGAGCTGTG 2649  
2621 CTGAAGCCCTGTGAGCCGATTAATGATCTCTCATGTATGTGTGCTG 2668

RESULT 10  
US-09-981-953A-3  
Sequence 3, Application US/0981953A  
GENERAL INFORMATION:  
PATENT No. 6689599  
APPLICANT: RACIE, LISA A.  
APPLICANT: TWINE, NATALIE C.  
APPLICANT: AGOSTINO, MICHAEL J.  
APPLICANT: WOLFMAN, NEIL

```
/ APPLICANT: MORRIS, ELIZABETH A.
/ TITLE OF INVENTION: NOVEL AGGREGANASE MOLECULES
/ FILE REFERENCE: 08702.0075-00000
/ CURRENT APPLICATION NUMBER: US/09/981,953A
/ PRIOR FILING DATE: 2001-10-18
/ PRIOR APPLICATION NUMBER: 60/242,317
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 3377
/ TYPE: DNA
/ ORGANISM: Unknown Organism
/ FEATURE:
/ OTHER INFORMATION: Description of unknown Organism: Nucleotide
/ OTHER INFORMATION: sequence of the aggreganase molecule
US-09-981-953A-3

Query Match      7.1%; Score 206.4; DB 4; Length 3377;
Best Local Similarity 49.3%; Pred. No. 2.1e-49;
Matches 704; Conservative 0; Mismatches 691; Indels 33; Gaps 5;

QY      1240 GGGAGAGATGGAGCTGTCATGACCAAGCCATCTTACTGACTGTGTGATATATGTTCC 1299
DB      1008 GAGAACGGTGTGGCTAACATGACACAGAGTGTCTATCACAGCTATGACATCTGCATC 1067
QY      1300 TGGAGAGATGAGCCCTGTGACACTTTGGATTGGACCCATTAAGTGAATGTGTAGTAA 1359
DB      1068 TACAAAGAACAAACCTTGCGGACACTAGGCTGCCCGGTGGGCGGAATGTGAGCCG 1127
QY      1360 TATCGAGCTGACGATTAATGAAGATACAGTCTTGGACTGCGCTTACCACTTGGCCAT 1419
DB      1128 GAGAAGAGCTGACGCTGATGAGACATTTGGCTGGCCACAGCGTTACCATTTGCCAC 1187
QY      1420 GAGTCTGACACACAATTTGGCATGATTTGATGAGAGAGGAGATGT-----GT 1470
DB      1188 GAGATCGGGACACATTTGGCATGAGACATGACGCGGTGGAAACAGCTGTGGGGCCGT 1247
QY      1471 AAAAAGTCCGAGGGCAACATCATGTCCCTTACATTTGGCAGAGACGAATGAGATCTTCTCC 1530
DB      1248 GGTCAAGAGCCCAAGCCAGCTCATGTGCTGCCCATTAACATGAAACCAACCCGTTCTGTG 1307
QY      1531 TGGTCAACCTTGGACCGCCAGATCTACACAAATTTCTAAGCACCGCTCAAGCTATCTGC 1590
DB      1308 TGGTCACTCTGACGCGTGTACATCAACGCTTTCTAGACTCGGGGCTGTGC 1367
QY      1591 CTGTGCTGATCAGCCAAAGCCTGTGAAGAAATACAAAGTATCTTGAAGAAATTTGCCAGAGAA 1650
DB      1368 CT---GAAACACCGACCCCGACAGAGACTTTGTGTACCCGACAGTGGACCGGGCCAA 1424
QY      1651 TTATATGATGCAAAACACAGTGCAGAGTGCAGTTGCGAGAGAAACCAAGCTCTGCATG 1710
DB      1425 GCCTACGATGACAGATGAGCAATGCGCTTTCAGCATGAGTCAAAATCGGCTGAGTAA 1484
QY      1711 CTGGAATTTAAAAAGACATCTGTAAAGCCCTGTGTGTCATGTATTTGGAAGAAATGT 1770
DB      1485 TACG-----GGAGGCTGTCAGACGAGCTGTGTGTCTGAGCAAGCAACCGGTGC 1535
QY      1771 GAGACTAAATTTATGCGACAGAGCAAGGCACAATTTGTGG-----CATGCATG 1821
DB      1536 ATCACCAACAGCATCCCGGCGCGGAGGCGACGCTGTGCACAGACACACATCGACAG 1595
QY      1822 TGGTCCCGGGAGAGACATGTGTGAATATGTGATGAAGAGCCCAAGCCCAATGTC 1881
DB      1596 GGGTGTGTCTACAAACGGGTCTGTGTCTCCCTTTGGGTCCGCGCCAGAGGATGTGACGGA 1655
QY      1882 CACTGTGCGGACTGTCTTCTTGTGTCCCATGTCTCAGAGACCTTGGGAGGGAGATATCT 1941
DB      1656 GCGTGGGGCGCGTGACTCCATGTGGGCTGACTGTGAGCGGACCTGTGGCGCGCGTGC 1715
QY      1942 CATAGAGTGCCTTGCACCAACCCCAAGCCATTCGATGAGAGGAAGTTCTGTGAGGC 2001
DB      1716 TCTTCTAGCCGTCACTGTGCAAGAGCCCAAGCCCAACATCGGGGCGAAGTACTGTGGGT 1775
```

```
QY      2002 TCCACTCGCACTGTGAAGCTCTGCAACAGTCAAGAAATGTCCCGGACAGTGTGACTTC 2061
DB      1776 GAGAGAGGCGGACACCGCTCTGTGAACACAGATGACTGTCCCGTGGCTCCAGAGACTTC 1835
QY      2062 CGTGTCTCATGTGTGCGGAGACCAACAGACAGCATTTGAGGGCGGCACTTCAAGTGG 2121
DB      1836 AAGAGATGCAAGTGTCTGAAATTTGACAGCATCCCTTTCGTTGGGAAATTTCAAGTGG 1895
QY      2122 AAGCTTACACTCAAGTAGAAGATCAGACTATGCAAACTCTACTGTATTCGAGAAAGGA 2181
DB      1896 AAAACGTACCGGGAGGGGGGCGTGAAGGCC---TCTCGCTCACTGTCTTACGGAAGGC 1952
QY      2182 TTTGATTTCTTCTTTCTTTTCTTTCCTTCAATTAAGTCAAAAGATGGGACTTCATGCTGAGAGAT 2241
DB      1953 TTCAACTTCTACAGGAGAGGGCGGACCGTGTGAGACGGGACACCTCGCGTCCAGAC 2012
QY      2242 AGCCGTAATGTTGTATATGATAGGATATGTGAGAGATTTGATGTGACAAATCTCTTGA 2301
DB      2013 ACGGTGACATTTGTGCTAGTGGCCGAATGCAAGCAGTGGGCTGCGACCGAGTCTTGCGG 2072
QY      2302 TCTGATGCTGTTGAAGACGCTGTGGGGTGTGTAACGGGAATPACTCAGCTGCAGATT 2361
DB      2073 TCCGACCTGCGGAGAGACAAAGTCCGAGTGTGTGGCGGTGAGCGCAGTGTCTCGAGACC 2132
QY      2362 CACAGGGGTCTCTACACCAAGACCAACCAACCAAGTATATCAATGTTCACATT 2421
DB      2133 ATCGAGGGGCTTTCAGCCACAGCTCACCTGGGGCGGGGTAGAGGATGTCTGTGATT 2192
QY      2422 CTTTCTGAGAGCCCGGAGATTCGCGATCTATGAAATGAAGTCTCTACCTCTCACTTTT 2481
DB      2193 CCAAAAGCTCTGTCACATCTTCAATCGAGATGAAACCTCTCTCAAGTCACTTGGCC 2252
QY      2482 GTGCGCAATGCGCTCAGAAAGTACTACTGAATGGGCACTGGACCGTGAAGCTGGCCGGC 2541
DB      2253 CTGAAGGAGACCAAGAGTCCCTGCTGTGAGAGGGGTGCCCGGAGACCCCGACGCCAC 2312
QY      2542 CGTACAAATTTTGGGCACTACTTTGACATACAGAGGTCTCTATATGAGCCCGAGAAC 2601
DB      2313 CCTTGCCTCTGAGTGGAGACCACTTTCAACTGCGACAGGGGCGACCAACAGGTCCAGAGC 2372
QY      2602 TTAATCGCTACGACCAACCAACGAGACATGATTTGGAGTCTGT 2649
DB      2373 CTGGAAGCCCTGGAGCCGATTAATGATCTCTCATGTGTGATGTGTG 2420

RESULT 11
US-09-392-184-5/C
/ Sequence 5, Application US/09392184
/ Patent No. 6395889
/ GENERAL INFORMATION:
/ APPLICANT: Robison, Keith E.
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
/ FILE REFERENCE: 5800-55
/ CURRENT APPLICATION NUMBER: US/09/392,184
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 5
/ LENGTH: 5357
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)_(5357)
/ OTHER INFORMATION: reprotolysin (ADAM family of metalloprotease)
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(5357)
/ OTHER INFORMATION: n = A,T,C or G
US-09-392-184-5

Query Match      7.1%; Score 204.6; DB 3; Length 5357;
```



```
QY 1360 TATCGAAGTGGCAAGATTAAATGAATACAGTCTTGGACCTTGACCAATTGCCAT 1419
DB 1371 GAGAGAGAGCTGGCAGCGTCAATGAGGACATTGGCTGGCCACAGCGTTCACTATGGCCAC 1430
QY 1420 GAGCTGGACACAACTTTGGCATGATTTCATGATGAGGAAGGGAACTATGCT-----GT 1470
DB 1431 GAGATGGGGACACATTCCTGGCATGAAACATGACGGCGTGGGAAACAGCTGTGGGGCCCGT 1490
QY 1471 AAAAAGTCCGAGGGGCAACATCATGTCCCTCACTATGGCAGGACGCAATGGAGTCTTCTCC 1530
DB 1491 GGTCAAGAGACCCAGCCAAAGTCAATGGCTGCCACATTACATGAAGACCAACCATTTCTGG 1550
QY 1531 TGGTCAACCTGGCAGCGGCCAGTATCTACACAAATTTCTAAGCACCGCTCAAGCTATCTCG 1590
DB 1551 TGGTCACTCCGACGCGGTGACTACATCACAGCTTTCTAAGACTCAAGGGCTCGGGGCTCTG 1610
QY 1591 CTGTGATGATGACCAAGCTGTGAAGGAATACAGATCTCTGAAGAAATTTGCCAGGAGAA 1650
DB 1611 CTTGAACACACGGGCGC---CCCAAGACAGGACTTGTGTATCCCAAGTGGCACCGGGCCAA 1668
QY 1651 TTATATGATGACAAACACACAGTCAAGTGGCACTTGGAGAGAAAGCCAAAGCTCTGCATG 1710
DB 1669 GCCTAAGATGACATGAGCAATCCCGCTTCAAGCATGAGTCAATCGCGTCACTGTGTA-- 1726
QY 1711 CTGGACTTTAAAAAGACATCTGTAAAGCCCTGTGTGCTCCATCTGTATTTGAGAGAAATGT 1770
DB 1727 -----AATACGGGAGGTCTGACAGCTGTGGTGTGTGAGCAAGAACCGGTGC 1778
QY 1771 GAGACTAAATTTATGACAGAGAGAGAGCAAAATTTGTGGGCA-----TGACATG 1821
DB 1779 ATCACCAACAGACATCCCGGCGCCAGGGGACGCTGTGCGACAGCAACCATCTGACAG 1838
QY 1822 TGGTGCAGGGGAGAGACATGTGTGAATATGTGATGAAGGGCCCAAGCCCATGTGC 1881
DB 1839 GGGTGGTGTCAAAACGGGCTGTGTCTCCCTTTGGGTCCGGGCTCAAGGGGTGTGACGGA 1898
QY 1882 CACTGTGTGCACTGTCTTCTTGTGTCCCATGTCTCAAGACCTGCGAGGGGGAGTATCT 1941
DB 1899 GCGTGGGGGCGGTGACCTCATGTGGGCGACTGACGCGGACCTGTGTGCGCGCGCTGTCC 1958
QY 1942 CATAGAGTGTGCTCTGACACCAACCCCAAGCCATGCGATGAGGGGAAGTTCTGTGAGGGC 2001
DB 1959 TCTTTAGCCGTGATCTGACAGACCCCAAGCCAAACATGCGGGGCAAGATCTGTGGGT 2018
QY 2002 TCCACTCGCACTCTGAAGCTCTGCAACAGTCAGAAATGTCCCGGAGCAGTGTGACTTC 2061
DB 2019 GAGAGAAAGCGGACCGGCTCTGCAACAGATGATGTCTCCCTGGCTCCAGGACTTC 2078
QY 2062 CGTGTCTCTCACTGTGTCCGAGCAACAGCAGATTCAGAGGGCGGCACTTCAAGTGG 2121
DB 2079 AAGGAAGTCAAGTGTCTGAATTTTGACAGCATCCCTTCCGTGGGAAATTTCTAAGTGG 2138
QY 2122 AAGCCTTACACTCAAGTAGAAGATCAGACTTAAGCAACTACTGATTCGAGAAAGA 2181
DB 2139 AAAAGCTACCGGGAGGGGCGGTGAAGGCC---TGCTCGCTACGTCCTTAGGGAAGGC 2195
QY 2182 TTTGATTTCTTCTTTCTTTTCTTTCATTAATGAATGAGACTTCATGCTCGAGAGAT 2241
DB 2196 TTCAAATTCTACACGGAAGGGGCGGACGCGTGTGTGAGCGGCACTCGCGTCCAGAC 2255
QY 2242 AGCCGTAATGTTGTATATAGTGGATATGTGAGAGATTTGATGTGACAAATGCTCTTGA 2301
DB 2256 ACGGTGGAATTTGCTCACTAGTGGCAATGCAAGCAAGTGGGCTGCGACCGAGTCCCTGGGC 2315
QY 2302 TCTGATGCTGTTGAAGCGTGTGGGGTGTGAAGGGGAATTAATCACTGACAGATTT 2361
DB 2316 TCCGACCTCGGGAGGACAAAGTCCGAGTGTGTGGGCTGTGAGCGGCACTTCGAGACC 2375
QY 2362 CACAGGGGTCTCTACACCAAGCACCAACCAACAGTATTTATCACTGTGACATTT 2421
DB 2376 ATCGAGGGGGTCTTCAAGCCAGCTCACTGGGGGCGGGTACGAGGATGTCTGTGATTT 2435
```

```
QY 2422 CCTTGGAGCCCGAGATTCGGCATCTATGAATGAACGTCTCACTCTCACTATTCT 2481
DB 2436 CCCAAAGGCTCCGTCACATCTTCAATCCAGATCTGAACCTCTCTCTCACTGTGGCC 2495
QY 2482 GNGCCAAATGCCCTGAGAAAGTACATCACTGAAATGGGCACTGGAACGGTGAAGTGGCCGGC 2541
DB 2496 CTGAAGGAGACACAGAGATCCCTGCTGCTGAGGGGCTGGCCGGGACCCCAAGCCCAAC 2555
QY 2542 CGGTACAAATTTTCGGGCACTACTTTGCACTACAGACGGTCTCTATATAGCCCGAGAAC 2601
DB 2556 CGTTCGCTCTAGCTGGGACCACTTTCAACTGCGACAGGGGCGAGCAAGGTCCAGAGC 2615
QY 2602 TTATTCCTACTGACACCAACAGACACTGATTTGAGAGTCTG 2649
DB 2616 CTGGAAGCCCTGGGACCGATTAATGATCATCTCATGTCAATGTGCTG 2663
```

```
RESULT 13
US-09-369-364A-6
; Sequence 6, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Taina L.
; APPLICANT: Hironaka, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 3218
; TYPE: DNA
; ORGANISM: Homo sapiens ADAMTS-7
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(3003)
US-09-369-364A-6
```

Query Match 6.3%; Score 182.6; DB 3; Length 3218;  
Best Local Similarity 50.8%; Pred. No. 1,9e+42;  
Matches 714; Conservative 0; Mismatches 649; Indels 42; Gaps 10;

```
QY 1258 CATGACCAAGCCCATCTTACTGACTGTGTGATATATGTTCTGTGAAGATGAGCCCTGT 1317
DB 1015 CATGACACTGCATCTGCTCTCCAGAAAGGACGTGTGTGAGCCATGAAACGGGCTGT 1074
QY 1318 GACACTTTGGGATTTGACCCATTAAGTGAATGTGTAGTAATATGCAAGCTGCAAGATT 1377
DB 1075 GAGACCCCTGGGACTGTCTCCATGTGTGGCGGCAATGTGCCAGCCGCAACCGACGTGCAGCATC 1134
QY 1378 AATGAAGATACAGGCTTGTGACTGGCTTCAACTATGGCCATGAGTGTGACACAACTTT 1437
DB 1135 AAGGAGGACAGGGGCTCCGCTGAGCTTCACTGTAGCCCAAGACTGGGCAAGTTTT 1194
QY 1438 GGCATGATTCATGATGAGAAAGGAACATGTGTAAAAAGTCCGAG-----GGCAACATC 1491
DB 1195 GGCATTTCAGATGAGGAAGGGGCAATGACTGTGAGCCCGTTGGGAAAGACCTTTTCAATC 1254
QY 1492 ATGTCCCTTCACTTGGAGAGACGCAATGAAGTCTTCTCTGTGTACCTGTGACGCCGCGAG 1551
DB 1255 ATGTCTCAACAGCTCTGTGAGAGCGCCGCTCCCTCACTGTGTCTGCGTGGACGCCGAG 1314
QY 1552 TATCTACCAAAATTTCTAAGGACCGCTCAAGCTATCTGCTTGTGATCAGCAAGGCT 1611
DB 1315 TATATACCAAGTTCTTGAACCGTGTGGTGGGCTGTGTCTGTGAGACCTCTCT---GCC 1371
QY 1612 GTGAAGGAATACAGTATCTGAGAAATTTCCAGGAGAAATTAATGATGACAAACACAG 1671
DB 1372 AAGGACATTTATGACTTCCCTCGGTGCGACCTGGCGTCTCTATGATGATGAAGCCAG 1431
QY 1672 TGCAAGTGGCACTTCCGAGAGAAAGCAAGCTCTGCACTGTGACCTTTAAAAAGACATC 1731
```





```
Db 1576 GCTGGGGGCGGTGACTCCATGAGGGGAGCTGACCGGACCTGTGCGCGCGCGGTCC 1635
QY 1942 CATAGGAGTCGCTCTGCAACCAACCCCAAGCCATCCGATGAGGGAAGTTCTGAGGCG 2001
Db 1636 TCTTCAAGTGTACAGTGGCAAGCCCAAGCCCAACCATGCGGGGCAAGTACTGTCTGGGT 1695
QY 2002 TCCACTCGCACTCTGAAGCTCTGCAACAGTCAGAAAATGTCCCGGGAAGTGTGACTTC 2061
Db 1696 GAGAGAGGGGGGACCGCTCTCTCCACACCGAGTACTGTCCCTGCTCCAGGACTTC 1755
QY 2062 CGTGTCTCAAGTGTGCGGACCAACAGCAGACATTCAGAGGGGGGCACTCAAGTGG 2121
Db 1756 AGAGAAAGTCAGTGTGTGATTTGAAGAGATCCCTTCCGTGGGAAATTTCAACAATG 1815
QY 2122 AAGCTTACATCTCAAGTAGAAGATCAGACTTATGCAAACTTACTGTATCCGAGAGGA 2181
Db 1816 AAAACGTAACGGGGAGGGGGCGTGAAGGCC--TGTCTGCTACGAGCTGAGGAAAGG 1872
QY 2182 TTTGATTTCTTCTTTCTTTCTTTGTCAAAATAAAGTCAAAAGATGGAGCTCCATGCTGGAGAT 2241
Db 1873 TTCACATTTTCAACGAGAGAGGGGCGAGCCGTGTGGAACGGGACACCTGCGCTCCAGAC 1932
QY 2242 AGCCGTAATGTTGTAATGATGGGATATGAGAGAGTTGATGAGCAATGTCTTGA 2301
Db 1933 ACGGTGACATTTGCGTCAGTGGCGAATGCAAGACAGTGGGCTGCAACGATCTTGCGC 1992
QY 2302 TCTGATGCTGTTGAAAGCGTCTGTGGGGGTGTGTAAACGGGAACTACAGCTGCAAGAT 2361
Db 1993 TCCGACCTGGGGAGGACAAAGTGCAGAGTGTGTGGGAGTGAACGGAGCTGTGCGAGAC 2052
QY 2362 CACAGGGGTCTCTACACCAAGACACACACCAACCAAGTATATCACTAGTGCACATT 2421
Db 2053 ATCGAAGGGGTCTTTCAGCCACGCTCACCTGGGGCGGGGTACAGAGATGTCTGTGAAT 2112
QY 2422 CCTTTCGAGGCCCGGAGTATCCGCATCTATGAATGAAGGTCTCTACTCTTCAATTCT 2481
Db 2113 CCCAAGGCTCGGTCCACATCTTCAATCCAGATCTGAACCTCTCTCTCACTGCTTGGCC 2172
QY 2482 GTGCGCAATGCTCTGAAAGGATCTACCTGAATGGGCACTGACCGTGAACCTGGCCGCG 2541
Db 2173 CTGAAGGAGAGACGAGAGTCCCTGTGTGAGGGGCTGCTGGGACCCCGACGCCAGC 2232
QY 2542 CGGTACAAATTTTTCGGGCACTATTTCGACTACAGCGGTCTCTATATAGCCCGAGAAC 2601
Db 2233 CGTGTGCTCTGTAGCTGGGACCACTTTCAACTGTGCAAGGGGCAAGCCAGGTCCAGAGC 2292
QY 2602 TTAATGCTACTGACCAACCAACGAGACACTGATTGTGAGCTGCTG 2649
Db 2293 CTCGAAGCCCTGGACCGATTAATGCACTCTCATGTCTATGTGCTG 2340

RESULT 15
US-09-369-364A-4
; Sequence 4, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Aptec, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hurskainen, Satochi
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09369,364A
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2848
; TYPE: DNA
; ORGANISM: Homo sapiens ADAMTS-6
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)..(2601)
```

```
; NAME/KEY: misc.feature
; LOCATION: (1369)
; OTHER INFORMATION: n = C
; NAME/KEY: misc.feature
; LOCATION: (1620)
; OTHER INFORMATION: n=C
US-09-369-364A-4

Query Match      5.0%; Score 144; DB 3; Length 2848;
Best Local Similarity 48.5%; Pred. No. 3.6e-31;
Matches 464; Conservative 0; Mismatches 481; Indels 12; Gaps 2;

QY 1726 GACATCTGAAGCCCTGTGTGTCATGTATTTGAGAGGAATGTGACTAAATTTATG 1785
Db 1390 GAGGTGTGAGAGACCTGTGTGTCTCAGCAAAACCAACCGCTGTGTCAACAGTAT 1449
QY 1786 CCAGCAGCAGAGAGGACATTTGTGGGATGACATGTGTGTCGGGGAGGACAGTGTG 1845
Db 1450 CCAGCAGCTGAGGGGACACTGTGTCAAACTGGGAATTTGAAAAAGGGTGTATTACG 1509
QY 1846 AAATATGTGAT-----GAAAGCCCAAGCCCAACCATGACCTGTGCGACTGG 1896
Db 1510 GGAATGTGTCTCTTTGGCACTTGCCCGCAGACATAGATGGGGCTGGGGTCCCTGG 1569
QY 1897 TCTTCTGTGTCCTTCCAGAGCTGTGGAGGAGGAGTATCTCATAGAGTGGCTTC 1956
Db 1570 TCACTATGGGAGAGTGAAGCAGGACCTGTGGGGAGGCGTNTCTCATCCCTAAGACAC 1629
QY 1957 TGCACCAACCCCAACCATGCGATGAGAGGAAATTTCTGTGAGGGGCTCCACTGCACTCTG 2016
Db 1630 TGTGACAGTCCAGCAGCTTCCGAGGTGAAAAATTTCTCTTGGGAAAAAGAAACGATAT 1689
QY 2017 AAGCTTCGAACAGTCAGAAATGTCCCGGGAAGTGTGACCTTCCGTGCTCAGTGT 2076
Db 1690 CGCTCTGTAAACACAGATTCATGCTCTTGGGTCCAGATTTTCGAGAGAAACAGTGT 1749
QY 2077 GCCGAGCAACAGAGACATTCAGAGGGGGGCACTCAAGTGAAGCCTTACACTCA 2136
Db 1750 GCGACTTTGACAAATATGCTTTTCCAGGAAAGTATTAATCTGGAACCCATATCT--- 1806
QY 2137 GTAGAGAGATCAGGACTTATGCAAACTACTGTATCGAGAAAGATTTGATTTCTTCT 2196
Db 1807 GGAAGTGGGGGTTAAACCTTTGTGATTAATCTGTGGCTGAAGGTTATATTTTCTACACT 1866
QY 2197 TCTTTGTCAATTAAGTCAAAAGATGGAATCCAGTCTCGAGAGATAGCCGTAATGTTGT 2256
Db 1867 GAACGTGCTCTCGCGGTATGATGATGGAACCAAGTGAATGCGGATTCATCGATATCTGC 1926
QY 2257 ATAGATGGGATATGAGAGAGTGTGATGACATATGCTTGTGATCTGATGCTGTGA 2316
Db 1927 ATCAATGGAAGATGCAACAGTATAGGCTGTATTAATTTTGGGATCTGATGCTAGGGA 1986
QY 2317 GACGTGTGGGGTGTGTAACGGGAAATTAATCAAGCTGCAAGATTCACAGGGGCTCTAC 2376
Db 1987 GATATATGTCAAGTGTGTGAGAGGGGCGGAGACATATGATGCAATGGAAGGTTCTTC 2046
QY 2377 ACCAAGCACACACCAACCAAGTATTAATCATGTGTACCATTCCTTCTGAGACCCGG 2436
Db 2047 AATGATTCATGCCCCAGGGGAGGCTACATGGAAGGTGACAGATCAAGAGGCTCTGTT 2106
QY 2437 AGTATCCGATCTATGAATAAGTCAAGTCTCTCACTCTCAATTTCTGTGCGCAATGCCCTC 2496
Db 2107 CACATTTGAAGTTAGAGAGTGTCCATGTCAAAAGACATATTTGCTTTAAATCTTAAGGA 2166
QY 2497 AGAAGTACTACTGGAATGGGCACTGACCGTGTGACTGGCCGGCCGGTACAAATTTTCG 2556
Db 2167 GATGATTAATTAATTAATGAGTGTGCTGTGACTATTAATGCTGCTTGAAGAAATTTGATGCT 2226
QY 2557 GGCCTACTTTCGACTACAGACGCTCTTAATATGAGCCCGAAGAACTTAATGCTACTGA 2616
Db 2227 GGGACAGCTTTTCAATTACAGAGACCAACTGATGAAACAGAACTCTTGAAGCTCTAGGT 2286
QY 2617 CCAACCAACGAGACACTGATTTGTGAGCTGCTGTTTACAGGAAGAACCCGGGTGT 2673
```

Db 2287 CCTACCTCAGAAATCTCATCGTCATGTTCTGCTTCAAGAACGAAATTTGGGAATT 2343

Search completed: September 9, 2005, 11:55:49  
Job time : 510 secs

This Page Blank (upside)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 9, 2005, 11:45:44 ; Search time 267 Seconds  
(without alignments)  
266.164 Million cell updates/sec

Title: US-09-981-151D-8  
Perfect score: 5236  
Sequence: 1 MKPRARGMGLAALMWLAQ.....LEAACQSAATAYIALAFLES 952

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3846.5	73.5	1224	4 US-09-930-872-4	Sequence 4, App1
2	3846.5	73.5	1224	4 US-10-217-774-4	Sequence 4, App1
3	1543.5	29.5	491	4 US-09-930-872-2	Sequence 2, App1
4	1543.5	29.5	491	4 US-10-217-774-2	Sequence 2, App1
5	1390	26.5	908	4 US-09-963-791-2	Sequence 2, App1
6	1319	25.2	757	4 US-09-963-791-24	Sequence 24, App1
7	1243	23.7	1104	4 US-09-961-953A-4	Sequence 4, App1
8	1188	22.7	859	3 US-09-369-364A-5	Sequence 5, App1
9	1179	22.5	997	3 US-09-369-364A-7	Sequence 7, App1
10	1057.5	20.2	1081	3 US-09-369-364A-17	Sequence 17, App1
11	1056	20.2	1882	3 US-09-369-364A-13	Sequence 13, App1
12	1022.5	19.5	950	4 US-09-321-987B-4	Sequence 4, App1
13	1022	19.5	770	4 US-09-981-953A-2	Sequence 2, App1
14	991	18.9	874	3 US-09-369-364A-15	Sequence 15, App1
15	984.5	18.8	967	4 US-09-130-491-2	Sequence 2, App1
16	982.5	18.5	949	4 US-09-568-559-2	Sequence 2, App1
17	969	18.5	2150	4 US-09-321-987B-2	Sequence 2, App1
18	965.5	18.4	2165	4 US-09-800-729-155	Sequence 15, App1
19	958.5	18.3	727	4 US-09-445-023A-12	Sequence 12, App1
20	949	18.1	1211	4 US-09-949-016-11401	Sequence 11401, A
21	948	18.1	969	4 US-09-321-987B-5	Sequence 5, App1
22	934	17.8	727	4 US-09-445-023A-1	Sequence 1, App1
23	933	17.8	1205	4 US-09-491-522-11	Sequence 11, App1
24	929.5	17.8	950	4 US-10-009-332-1	Sequence 1, App1
25	923	17.6	1211	4 US-09-491-522-5	Sequence 5, App1
26	903	17.2	608	4 US-09-130-491-13	Sequence 13, App1
27	885.5	16.9	930	3 US-09-369-364A-2	Sequence 2, App1

28	878	16.8	930	4 US-09-122-126B-15	Sequence 15, App1
29	878	16.8	930	4 US-09-634-286A-15	Sequence 15, App1
30	878	16.8	930	4 US-10-247-685-15	Sequence 15, App1
31	856.5	16.4	837	4 US-09-122-126B-2	Sequence 2, App1
32	856.5	16.4	837	4 US-09-634-286A-2	Sequence 2, App1
33	856.5	16.4	837	4 US-10-247-685-2	Sequence 2, App1
34	823.5	15.7	905	3 US-09-369-364A-9	Sequence 9, App1
35	778.5	14.9	551	4 US-09-130-491-16	Sequence 16, App1
36	776.5	14.8	589	4 US-09-963-791-12	Sequence 12, App1
37	705.5	13.5	438	4 US-09-963-791-22	Sequence 22, App1
38	675.5	12.9	518	3 US-09-369-364A-22	Sequence 22, App1
39	607	11.6	481	4 US-09-130-491-8	Sequence 8, App1
40	578.5	11.0	507	4 US-09-963-791-10	Sequence 10, App1
41	550	10.5	1039	4 US-09-949-016-7859	Sequence 7859, App1
42	507.5	9.7	356	4 US-09-963-791-20	Sequence 20, App1
43	476.5	9.1	446	4 US-09-784-358-4	Sequence 4, App1
44	476.5	9.1	724	4 US-09-784-358-8	Sequence 8, App1
45	476.5	9.1	845	4 US-09-784-358-12	Sequence 12, App1

ALIGNMENTS

RESULT 1									
US-09-930-872-4									
; Sequence 4, Application US/09930872									
; Patent No. 6448388									
; GENERAL INFORMATION:									
; APPLICANT: Fiddie, Carl Johan									
; APPLICANT: Hilburn, Erin									
; FILE OF INVENTION: No. 6448388e1 Human Proteases and Polynucleotides Encoding the San									
; TITLE REFERENCE: LEX-0219-USA									
; CURRENT APPLICATION NUMBER: US/09/930,872									
; PRIOR FILING DATE: 2001-08-14									
; PRIOR APPLICATION NUMBER: US 60/225,852									
; PRIOR FILING DATE: 2000-08-16									
; NUMBER OF SEQ ID NOS: 5									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 4									
; LENGTH: 1224									
; TYPE: PRT									
; ORGANISM: homo sapiens									
US-09-930-872-4									
Query Match 73.5%; Score 3846.5; DB 4; Length 1224;									
Best Local Similarity 75.4%; Pred. No. 0;									
Matches 738; Conservative 25; Mismatches 73; Indels 143; Gaps 13;									
QY	1	MKPRARGMGLAALMWLAQVAQVSPGRSHQGRNGSGOLEASPPRLSRGPRRLTAMS	60						
DB	1	MKPRARGMGLAALMWLAQVAQAP-----ACAMG	31						
QY	61	PLFSAGTCYRHGTRSGASNEPPERPASSSTRGAAGLDGKGRMDGAKNSQQTNTGTEND	120						
DB	32	PAAAA-----PSSPVPRPPPAERPG-----WMEKG-----	58						
QY	121	TLHVLQYVLVAAYEVDHGRGVSHRIMHQRRAVAVASEVSLRLKGPDPHMDL	180						
DB	59	-----EYDVSAYEVDHGRGVSHRIMHQRRAVAVASEVSLRLKGRSHDHVDL	112						
QY	181	RTSSSLVABGFIYQTLGKTGTSVQTLPPEDFCFYGSLSRSHNSPSHGKFCGSTRLL	240						
DB	113	RTSSSLVABGFIYQTLGKTGTSVQTLPPEDFCFYGSLSRSHNS-SVALSTCGLSGMI	171						
QY	241	KLCNSGKCRPDSVDFPAACAEHNSRRFGR-----HYKKPYTQVBA-DLCGLYCI	291						
DB	172	R-----TEADVFLRPLPSHLISWKL-GRAAQSSPSHVLTKSTTEHAPGASVAVT	222						
QY	292	ABGDFPFFS--LSNKYKDGTPCSEDSGRANCIDICLSVSTSAHMPQPKEDFLTPDE	349						
DB	223	SRTWELAHQPLHSSDLRLGLP--OKQHFC-----GRKKKAPQPKEDFLTPDE	270						
QY	350	YKSCLRHRSLLRSHNREINAVETLVVVDKKMQNHGHNITTYVYLTILMVSALEPKD--	407						

```
Db 271 YKSLHRSKSLRSHRNEELNVELTVVDDKKMOMNGHENITTYVLTJLNMVSALFKDGT 330
QY 408 -----GLMGKDGTRHDAHLLTGLD 427
Db 331 IGGNINIAIVGLILLEDEQPGVLISHHADHTLSPFCQMOSGLMGKDGTRHDAHLLTGLD 390
QY 428 ICSWNEPCDITGLFAPISGMCSKYRSCCTINEDTGLAFTIAHESGHNFGMIHDEGNNC 487
Db 391 ICSWNEPCDITGLFAPISGMCSKYRSCCTINEDTGLAFTIAHESGHNFGMIHDEGNNC 450
QY 488 KKESEGNISPTLAGRNVSPSCSRQYLHKFLSTAQAICLAOPKPYKEYKPEKLPGE 547
Db 451 KKESEGNISPTLAGRNVSPSCSRQYLHKFLSTAQAICLAOPKPYKEYKPEKLPGE 510
QY 548 LYDANTOCKMOPGEKAKLCLMDPKDICKALWCHRIGRKCEKTFMPAAEGTICGHDMMCR 607
Db 511 LYDANTOCKMOPGEKAKLCLMDPKDICKALWCHRIGRKCEKTFMPAAEGTICGHDMMCR 570
QY 608 GGCVCYKGDGEPKPTGHGMSDMSWSPCSRTCCGGVSHRSRLCTNPKPSHGKFCGSGTR 667
Db 571 GGCVCYKGDGEPKPTGHGMSDMSWSPCSRTCCGGVSHRSRLCTNPKPSHGKFCGSGTR 630
QY 668 TLKLCNSOKCPRSDVDFRAQCAEHNSRRFRGRHYKMKPYTOVEDODLCKLYCIAEGPDF 727
Db 631 TLKLCNSOKCPRSDVDFRAQCAEHNSRRFRGRHYKMKPYTOVEDODLCKLYCIAEGPDF 690
QY 728 FFSLSNKVKDGTPCSEDSRNVCIDGICERVGCDNVLGSDAEDVCGVCNGNNSACTIHNG 787
Db 691 FFSLSNKVKDGTPCSEDSRNVCIDGICERVGCDNVLGSDAEDVCGVCNGNNSACTIHNG 750
QY 788 LYTKHHNTQYHYMNTIPSGARSIRIYEMNVSTSYISVNALRRYYLNGHMTVDWPGRYK 847
Db 751 LYTKHHNTQYHYMNTIPSGARSIRIYEMNVSTSYISVNALRRYYLNGHMTVDWPGRYK 810
QY 848 FSGTTFDYSRYNEENLIATGPTNETLIVELLFQGRNPGVAMEYSMPRLGTEKOPPAOP 907
Db 811 FSGTTFDYSRYNEENLIATGPTNETLIVELLFQGRNPGVAMEYSMPRLGTEKOPPAOP 870
QY 908 SYTMAIVRSECSVSCGGG 926
Db 871 SYTMAIVRSECSVSCGGG 889

RESULT 2
US-10-217-774-4
; Sequence 4, Application US/10217774
; Patent No. 6734007
; GENERAL INFORMATION:
; APPLICANT: Frittle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. 6734007el Human Proteases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/10/217,774
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/930,872
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastrSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1224
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-217-774-4

Query Match 73.5%; Score 3846.5; DB 4; Length 1224;
Best Local Similarity 75.4%; Prid. No. 0;
Matches 738; Conservative 25; Mismatches 73; Indels 143; Gaps 13;

QY 1 MRPBARGMGLAALMWLLAQVAEQVSPGRSHQKGNNGSQLEASPPRLLSRGPRLTAMS 60
```

```
Db 1 MRPBARGMGLAALMWLLAQVAEQAP-----ACAAG 31
QY 61 PLFSAGTCVRHGTGRSGASAMEPERPASSSTRGAAGDGGKRDMDGANNHRSQCTNTGTENG 120
Db 32 PAAAA-----FGSPVPRPPPAERPG-----MMEG----- 58
QY 121 TLHVLTOYDLSAYAVDHRGDVYSHIIMHQRRRAVAVSEVSLHLRLKGRPHFMDL 180
Db 59 -----EVDLSAYAVDHRGDVYSHIIMHQRRRAVAVSEVSLHLRLKGRPHFMDL 112
QY 181 RTSSSLVAPGFLVOTLGTGTSVOTLPREDCFYQSLRSRNSPSHGKRCESGTRTL 240
Db 113 RTSSSLVAPGFLVOTLGTGTSVOTLPREDCFYQSLRSRNS-SVALSTCGSLSGMI 171
QY 241 KLCNSOKCPRSDVDFRAQCAEHNSRRFRGR-----HYMKKYTQVEA-DLCKLYCI 291
Db 172 R-----TEADYFLRLPRLSHWLK-GRAAQSSSPHVLTXKSTEPHAAGASEVLVT 222
QY 292 AEGPDFPS--LSNKVKDGTPCSEDSRNVCIDGICELSVSTSAHMPORPKEDLFLPDE 349
Db 223 SRTWELAQPLHSSDLRLGLP--OKHFC-----GRKKYMPORPKEDLFLPDE 270
QY 350 YKSLHRSKSLRSHRNEELNVELTVVDDKKMOMNGHENITTYVLTJLNMVSALFKD-- 407
Db 271 YKSLHRSKSLRSHRNEELNVELTVVDDKKMOMNGHENITTYVLTJLNMVSALFKDGT 330
QY 408 -----GLMGKDGTRHDAHLLTGLD 427
Db 331 IGGNINIAIVGLILLEDEQPGVLISHHADHTLSPFCQMOSGLMGKDGTRHDAHLLTGLD 390
QY 428 ICSWNEPCDITGLFAPISGMCSKYRSCCTINEDTGLAFTIAHESGHNFGMIHDEGNNC 487
Db 391 ICSWNEPCDITGLFAPISGMCSKYRSCCTINEDTGLAFTIAHESGHNFGMIHDEGNNC 450
QY 488 KKESEGNISPTLAGRNVSPSCSRQYLHKFLSTAQAICLAOPKPYKEYKPEKLPGE 547
Db 451 KKESEGNISPTLAGRNVSPSCSRQYLHKFLSTAQAICLAOPKPYKEYKPEKLPGE 510
QY 548 LYDANTOCKMOPGEKAKLCLMDPKDICKALWCHRIGRKCEKTFMPAAEGTICGHDMMCR 607
Db 511 LYDANTOCKMOPGEKAKLCLMDPKDICKALWCHRIGRKCEKTFMPAAEGTICGHDMMCR 570
QY 608 GGCVCYKGDGEPKPTGHGMSDMSWSPCSRTCCGGVSHRSRLCTNPKPSHGKFCGSGTR 667
Db 571 GGCVCYKGDGEPKPTGHGMSDMSWSPCSRTCCGGVSHRSRLCTNPKPSHGKFCGSGTR 630
QY 668 TLKLCNSOKCPRSDVDFRAQCAEHNSRRFRGRHYKMKPYTOVEDODLCKLYCIAEGPDF 727
Db 631 TLKLCNSOKCPRSDVDFRAQCAEHNSRRFRGRHYKMKPYTOVEDODLCKLYCIAEGPDF 690
QY 728 FFSLSNKVKDGTPCSEDSRNVCIDGICERVGCDNVLGSDAEDVCGVCNGNNSACTIHNG 787
Db 691 FFSLSNKVKDGTPCSEDSRNVCIDGICERVGCDNVLGSDAEDVCGVCNGNNSACTIHNG 750
QY 788 LYTKHHNTQYHYMNTIPSGARSIRIYEMNVSTSYISVNALRRYYLNGHMTVDWPGRYK 847
Db 751 LYTKHHNTQYHYMNTIPSGARSIRIYEMNVSTSYISVNALRRYYLNGHMTVDWPGRYK 810
QY 848 FSGTTFDYSRYNEENLIATGPTNETLIVELLFQGRNPGVAMEYSMPRLGTEKOPPAOP 907
Db 811 FSGTTFDYSRYNEENLIATGPTNETLIVELLFQGRNPGVAMEYSMPRLGTEKOPPAOP 870
QY 908 SYTMAIVRSECSVSCGGG 926
Db 871 SYTMAIVRSECSVSCGGG 889

RESULT 3
US-09-930-872-2
; Sequence 2, Application US/09930872
; Patent No. 6448388
; GENERAL INFORMATION:
```

```
/ APPLICANT: Fridde, Carl Johan
/ APPLICANT: Hilbun, Erin
/ TITLE OF INVENTION: No. 6448388el Human Proteases and Polynucleotides Encoding the Sa
/ FILE REFERENCE: LEX-0219-USA
/ CURRENT APPLICATION NUMBER: US/09/930,872
/ CURRENT FILING DATE: 2001-08-14
/ PRIOR FILING DATE: 2000-08-16
/ PRIOR APPLICATION NUMBER: US 60/225,852
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PaateSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 491
/ TYPE: PRT
/ ORGANISM: homo sapiens
/ US-09-930-872-2

Query Match      29.5%; Score 1543.5; DB 4; Length 491;
Best Local Similarity 57.7%; Pred. No. 2.2e-129;
Matches 333; Conservative 26; Mismatches 75; Indels 143; Gaps 13;

QY      1 MKPRAGMKGALAMLLAQAQVSPGSHQGRNGSGQLASPRLLSRGPRRLTAMS 60
DB      1 MKPRAGMKGALAMLLAQAQVSPGSHQGRNGSGQLASPRLLSRGPRRLTAMS 60
QY      61 PLPSAGTCVHRGTRSGSAMPERPASSSTRGAAGLDGKGRDMDAGNHSQQTNTGTENQ 120
DB      32 PAAAA-----PGSPSVPRPPPAERPG-----MMKKG-----ACAMG 31
QY      121 TLHVLTOYDLVSAVEYDHRGDYVSHIMHQRRAVAVSEVSLHLRLKGRPHDFMDL 180
DB      59 -----EYDLVSAVEYDHRGDYVSHIMHQRRAVAVSEVSLHLRLKGRSHDFHVDL 112
QY      181 RTSSSLVAGFIVQTLGKTGTSVQTLPPEDPCFYOGSLSRHNSPSHGKPFCEGSTRLL 240
DB      113 RTSSSLVAGFIVQTLGKTGTSVQTLPPEDPCFYOGSLSRHNS-SVALSTCGLSGMI 171
QY      241 KLCNSQKCPRSDVDFRAQCAEHNSRRFRGR-----HYKKPYTOVEA-DLCKLYCI 291
DB      172 R-----TEADYFLRLPLPSHLNWL-GRAGQSSPSHVLKSTEPHAPGASEVLVT 222
QY      292 AEGFDFPFS--LSNKYKDGTPCSEDSRNVCIIDICELSVSTSAHNPORPKEDFLTPDE 349
DB      223 SRTWELAHQPLHSSDLRLGP---QKHFC-----GRRKKWPORPKEDFLTPDE 270
QY      350 YKSCLRHKSLSLRSHNEELAVETLVVVDKQKQNHGHEHNTTYVLTILNMSALFKD-- 407
DB      271 YKSCLRHKSLSLRSHNEELAVETLVVVDKQKQNHGHEHNTTYVLTILNMSALFKDGT 330
QY      408 -----GLMKDQTRHDAIILITGLD 427
DB      331 IGGNINIAIVGLILLEDEQGLVISHHADHTLSSFCQWQSGLMGKDGTRHDAIILITGLD 390
QY      428 ICSWKNEPCDTLGFAPISGMSKYSRCTINEDTGLGLAFTIAHSGHNGMTHDGGNMC 487
DB      391 ICSWKNEPCDTLGFAPISGMSKYSRCTINEDTGLGLAFTIAHSGHNGMTHDGGNMC 450
QY      488 KXSEGINMPTLAGRNGVFSWSPCSROYLHKFLSTAQ 524
DB      451 KXSEGINMPTLAGRNGVFSWSPCSROYLHKFLRSYK 487

RESULT 4
US-10-217-774-2
/ Sequence 2, Application US/1021774
/ GENERAL INFORMATION:
/ APPLICANT: Fridde, Carl Johan
/ APPLICANT: Hilbun, Erin
/ TITLE OF INVENTION: No. 67344007el Human Proteases and Polynucleotides Encoding the
/ FILE REFERENCE: LEX-0219-USA
/ CURRENT APPLICATION NUMBER: US/10/217,774
/ CURRENT FILING DATE: 2002-08-12
```

```
/ PRIOR APPLICATION NUMBER: US/09/930,872
/ PRIOR FILING DATE: 2001-08-14
/ PRIOR APPLICATION NUMBER: US 60/225,852
/ PRIOR FILING DATE: 2000-08-16
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PaateSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 491
/ TYPE: PRT
/ ORGANISM: homo sapiens
/ US-10-217-774-2

Query Match      29.5%; Score 1543.5; DB 4; Length 491;
Best Local Similarity 57.7%; Pred. No. 2.2e-129;
Matches 333; Conservative 26; Mismatches 75; Indels 143; Gaps 13;

QY      1 MKPRAGMKGALAMLLAQAQVSPGSHQGRNGSGQLASPRLLSRGPRRLTAMS 60
DB      1 MKPRAGMKGALAMLLAQAQVSPGSHQGRNGSGQLASPRLLSRGPRRLTAMS 60
QY      61 PLPSAGTCVHRGTRSGSAMPERPASSSTRGAAGLDGKGRDMDAGNHSQQTNTGTENQ 120
DB      32 PAAAA-----PGSPSVPRPPPAERPG-----MMKKG-----ACAMG 31
QY      121 TLHVLTOYDLVSAVEYDHRGDYVSHIMHQRRAVAVSEVSLHLRLKGRPHDFMDL 180
DB      59 -----EYDLVSAVEYDHRGDYVSHIMHQRRAVAVSEVSLHLRLKGRSHDFHVDL 112
QY      181 RTSSSLVAGFIVQTLGKTGTSVQTLPPEDPCFYOGSLSRHNSPSHGKPFCEGSTRLL 240
DB      113 RTSSSLVAGFIVQTLGKTGTSVQTLPPEDPCFYOGSLSRHNS-SVALSTCGLSGMI 171
QY      241 KLCNSQKCPRSDVDFRAQCAEHNSRRFRGR-----HYKKPYTOVEA-DLCKLYCI 291
DB      172 R-----TEADYFLRLPLPSHLNWL-GRAGQSSPSHVLKSTEPHAPGASEVLVT 222
QY      292 AEGFDFPFS--LSNKYKDGTPCSEDSRNVCIIDICELSVSTSAHNPORPKEDFLTPDE 349
DB      223 SRTWELAHQPLHSSDLRLGP---QKHFC-----GRRKKWPORPKEDFLTPDE 270
QY      350 YKSCLRHKSLSLRSHNEELAVETLVVVDKQKQNHGHEHNTTYVLTILNMSALFKD-- 407
DB      271 YKSCLRHKSLSLRSHNEELAVETLVVVDKQKQNHGHEHNTTYVLTILNMSALFKDGT 330
QY      408 -----GLMKDQTRHDAIILITGLD 427
DB      331 IGGNINIAIVGLILLEDEQGLVISHHADHTLSSFCQWQSGLMGKDGTRHDAIILITGLD 390
QY      428 ICSWKNEPCDTLGFAPISGMSKYSRCTINEDTGLGLAFTIAHSGHNGMTHDGGNMC 487
DB      391 ICSWKNEPCDTLGFAPISGMSKYSRCTINEDTGLGLAFTIAHSGHNGMTHDGGNMC 450
QY      488 KXSEGINMPTLAGRNGVFSWSPCSROYLHKFLSTAQ 524
DB      451 KXSEGINMPTLAGRNGVFSWSPCSROYLHKFLRSYK 487

RESULT 5
US-09-963-791-2
/ Sequence 2, Application US/09963791
/ Patent No. 6649399
/ GENERAL INFORMATION:
/ APPLICANT: Donoho, Gregory
/ APPLICANT: Turner, C. Alexander Jr.
/ APPLICANT: Friedlich, Glenn
/ APPLICANT: Scoville, John
/ APPLICANT: Zambrowicz, Brian
/ APPLICANT: Sands, Arthur T.
/ TITLE OF INVENTION: No. 6649399el Human Proteases and Polynucleotides Encoding the San
/ FILE REFERENCE: LEX-0105-USA
/ CURRENT APPLICATION NUMBER: US/09/963,791
/ CURRENT FILING DATE: 2000-12-08
/ PRIOR APPLICATION NUMBER: US 60/169,769
```





```
RESULT 7
US-09-981-953A-4
/ Sequence 4, Application US/09981953A
/ Patent No. 6689599
/ GENERAL INFORMATION:
/ APPLICANT: RACIE, LISA A.
/ APPLICANT: TWINE, NATALIE C.
/ APPLICANT: AGOSTINO, MICHAEL J.
/ APPLICANT: WOLPMAN, NEIL
/ APPLICANT: MORRIS, ELISABETH A.
/ TITLE OF INVENTION: NOVEL AGGREGANASE MOLECULES
/ FILE REFERENCE: 08702.0075-00000
/ CURRENT APPLICATION NUMBER: US/09/981,953A
/ CURRENT FILING DATE: 2001-10-18
/ PRIOR APPLICATION NUMBER: 60/242,317
/ PRIOR FILING DATE: 2000-10-20
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 1104
/ TYPE: PRT
/ ORGANISM: Unknown Organism
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism: Amino acid
/ FEATURE:
/ OTHER INFORMATION: sequence of the aggreganase molecule
/ NAME/KEY: MOD_RES
/ LOCATION: (1104)
/ OTHER INFORMATION: Any amino acid
US-09-981-953A-4

Query Match      23.7%; Score 1243; DB 4; Length 1104;
Best Local Similarity 31.4%; Pred. No. 6,6e-102;
Matches 295; Conservative 133; Mismatches 317; Indels 194; Gaps 24;

QY 84 PASSSTRGAAGLDGKRDNDDEAGNHSQQTNTGTENQTLAVLTQYDLVSAVEYDHNGDVT 143
DB 3 PACQILRMALAL-GLGLMEFVTHAFPSQ-----DEFLSLESYTIAPTRVDHNGALL 54
QY 144 SHEIMHQRRAVAVSEVESLHLRLKGRPHDFHMDLRTSSSLVADGPIVQTLGKTGYKS 203
DB 55 AFSPPRRQRGRGTGATAESRLFEYKVASPSTHPLMLTRSSRLLAGHVSVEYTRREGLAM 114
QY 204 VQTLPPEDCFYQGSLSRSHNS-----PSHGKFCGSGSTR 238
DB 115 QRARPH--CLYAGHLQQAASSSHVAISTCGGLHGLIVADEEYLIETPLHGP--KGS-- 168
QY 239 TLKLCNSQKCPRDS--VDFAAQ-----CAEHSRRFRGRHYKWKPYTQVEADLC 286
DB 169 -----RSPESRPHVYVYKSSLSLRHPLDTCAGYRDEKPKMGRPMWLRTLKPPRAR-- 218
QY 287 KLYCIAEGDFPFPSLSNKVKYDGTPCSEDSRNVCIDGICELSVVSTSAHMPQRPKEDLFTL 346
DB 219 -----PLGNETERGQP-----GL----- 231
QY 347 PDEYKSLAHKSKLSLRSHNEELAVETLVVVDKMMQNHENITTYVLTILMVSALPK 406
DB 232 -----KQSVSR-----ERYVETLVVADKMMVAYHGRDVEQYVALIMNIVAKLQ 276
QY 407 DGLMG-----KDG-- 414
DB 277 DSSLGTVNIIIVTRLILLTEDEQPLEITTHAGKSLDSFCCKMOKSYNHSGHGNAIENKV 336
QY 415 TRHDHAILLTGLDICSWKNEPCDTLGPAPISGMCKSYRSCCTINEDTGLGIAPTIASHG 474
DB 337 AHHDTAVLLITRYDICIYKWKPCGTLGLAPGVGCERERSCSVVEDIGLATAFTIAEIGH 396
QY 475 NGCMTHDGGNMC--KXSEGNIMSPTLAGRNVFSPSCSROYLHKPLSTADAITLAAQ 531
DB 397 TFGMNHDSVGNSCGARGDPAKLMMAHITMKNPFWVSSCSRDIYITSFIDSLGICLNNR 456
```

```
QY 532 PRVKEKYYPEKLPBELYDANTQCKMKGFEKAKLCMLDFKKDICALMCHRIGRKCEYK 591
DB 457 P-PRODFVYVTVAPQOAYDADBCRFQHGKVRCKQYK--EVCSELWCLSKSNRICTNS 512
QY 592 MPAAEGTIC-GHDM--WRRGQCYKYGDDEGKPLTHGHMSDMSWSFGCRTLGGCVSHS 647
DB 513 IPAAGTILCQTHITIDKMGWCYKRVCPVFGSR--PEGVDGAWGWPMPWDGCSRTGGGVSSS 571
QY 648 RLCTNPKPSHGKFCGSGSTRTLKLCNSQKCPRDSVDFAAQCAEHSRRFRGRHYKWKPY 707
DB 572 RHCDSRPRTIGSKYCLGERRRHRSCTNTDCCPFGSQDFRVCSEFSDIPFRKGFYKMKY 631
QY 708 TQVEDODLCKLYCIAEGDFPFPSLSNKVKYDGTPCSEDSRNVCIDGICERVGCDNYLGS 767
DB 632 -RGGVYKACSLTCLABGFNFYTERAAAVVDGTPRCRPFVDICVSGECKHVGCDRYLGS 690
QY 768 VEDVCGVCGNNSACTIHRLYTKHHNTQYHMTTISGANSIKLIYENNVSTSYISVN 827
DB 691 REDKCRVCGDGSACETIEGVFSPASPGAGYEDVVMIPKGSVHIFIODLNTLSHLALKG 750
QY 828 ALRYYLNGHMTVDPMPGRKYFGTTFDYRSYNEPENLIATGPTRETLIVELLFOGRNG 887
DB 751 DQSLILBSGLPCTPQPHRLPLAGTTPLQLRQGPDOVQSLALGPIINSLIWMYIARTE 810
QY 888 VAMEXSMPLRGTCKQPPAOPSYTMAIVR-SECSVSCGG 925
DB 811 LMYRFNAP-IARDSLP-----YSMHYAPMTKCSAOCAG 844

RESULT 8
US-09-369-364A-5
/ Sequence 5, Application US/09369364A
/ Patent No. 6391610
/ GENERAL INFORMATION:
/ APPLICANT: Apte, Suneel
/ APPLICANT: Hurskainen, Tiina L.
/ APPLICANT: Hirohata, Satoshi
/ TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
/ FILE REFERENCE: 26473/4007/10-30-00
/ CURRENT APPLICATION NUMBER: US/09/369,364A
/ CURRENT FILING DATE: 1999-08-06
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 859
/ TYPE: PRT
/ ORGANISM: Homo sapiens ADAMTS-6
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (450)
/ OTHER INFORMATION: Xaa = L
US-09-369-364A-5

Query Match      22.7%; Score 1188; DB 3; Length 859;
Best Local Similarity 31.4%; Pred. No. 3.7e-97;
Matches 284; Conservative 132; Mismatches 289; Indels 200; Gaps 25;

QY 108 HNSQQTNTGTENQTLAVLTQYDLVSAVEYDHNGDYVSHIIM--HQRRRAV-----AVSE 161
DB 22 HSDHLSYSSQDEFTLYEHTYQTLPIRDONGARLSFTVKNDDKSRRRSMOPIDPOQA 81
QY 162 VESLHLRLKGRPHDFHMDLRTSSSLVADGPIVQTLGKTGTSVQTLPP-----DFCFY 215
DB 82 VSKLFKLSAYKHHHMLNTLNTDVSAGFTYEVYNGKQ-----PQMKHDFPNDCHY 133
QY 216 QGSLRSHRNSPSHGKFCGSGSTRTLKLCNSQKCPRDSVDFAAQCAE--HNSRRFRGRHYK 274
DB 134 TGYLDOR-----STTKVALSN-----CVGLHGVATATEDEEYF 166
QY 275 WKPYTQVEADLCKLYCIAEGDFPFPSLSNKVKYDGT-----CSDSNRNVCIDGICELSV 328
DB 167 IEPKNTTED-----SKHFSY-----ENGHPHVIYKKSALQQRHLVDHSHCGVSD 211
```



```

; GENERAL INFORMATION:
; APPLICANT: Aptec, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satochi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ. ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ. ID NO 17
; LENGTH: 1081
; TYPE: PRT
; ORGANISM: Homo sapiens ADAMTS-10
US-09-369-364A-17

Query Match      20.2%; Score 1057.5; DB 3; Length 1081;
Best Local Similarity 30.2%; Pred. No. 2.6e-85;
Matches 265; Conservative 120; Mismatches 286; Indels 207; Gaps 26;

QY 164 SLHLRLKGG--PRHDFH-----MDLSTSSIVAPGFIVQTIGTKTSKV 204
DB 35 SRHL-LFGAARHGSHSRVPPPLQSGLAHFLNLTSSRLLAGRVSVETWTRBGLAMQ 93
QY 205 QTLPPEDFCFYQGSLSRSHRS-----PSHGKFCGEGSTRT 239
DB 94 RAARPH--CLYAGHLQGAASSSHVAISTCGHLGLIVADEEYLIIEPLHGGP--KGS--- 146
QY 240 LKLCNSQKCRDS---VDFRAA-----QCAENHSRRPRGHHYKMYKRYTOVEADLCK 287
DB 147 -----RSPDESGPHCVYKRSSLRHPHLDTACCVBDEKPMKGPWWLRTLKPPRA-- 196
QY 288 LYCIAEGDFPFSLNSNVKDTPCSEDSRNVCIDIGELSVSTSAAMPPEKDEFLTP 347
DB 197 -----PLGNTERGQP-----GL----- 209
QY 348 DEYKSLRHRSLSLRSHNELNVEITLVVDKMMQNHENITTYVLTILNVSALFKD 407
DB 210 -----KRSVSR-----ERYETWIDVADKMMVAHGRDVEDQYVLAIMNIVAKLFQD 255
QY 408 GLMG----- 415
DB 256 SSGSTVNILVTRLILTEDQPLEITHHAGKSLDSPCKMQKSTVNSHGMAIPENGVA 315
QY 416 RHDHAILLGLDTCMKNEPCDTLGFAPISGMSKYSCITINBDTGGLAFTIAHESGN 475
DB 316 NHDVALITRYDICTYKNCCTGLARMA-ECVSAEBAASMKTLAATVHHCHETIGHT 374
QY 476 FGMIHDEGNMC--KKEGNNISPTLAGRNGVFSWSPCSROYLHKFLSTAQAICLADP 532
DB 375 FGMNHGVGNSCGARQDPAKLAHAHITMTNTNPPVWSSCNRDYITSLDGLGCLNRP 434
QY 533 KPYKEYYPEKLPGELYDANTQCKMFGKAKLCMLDFKDKICAKMCHIRGKCTEKM 592
DB 435 -PRODFYVPTVAAGQADADQCFQHGVSROCKY--EVCSELMCLSKSRCTINSI 490
QY 593 PALEGTC-GHDM--WCRGGQCVKYGDEBPKPTHGMSDMSMSPCSRCCGGVSHSR 648
DB 491 PAABGTLCTQHHTIDKGCYKRVCPFGSR-PEGVDGAGMPTTPGDGSSRTCCGGVSSSR 549
QY 649 LCTNPKPSHGKFCGEGSTRTLKLNSQKCPDSVDVFAAQAENHSRRFRGRHYKMPYT 708
DB 550 HCSPPRTTIGKCYCLGERRRHRSCNTDDCPGSGDPFEVQCAEFDJLPPFGKPYKMTY- 608
QY 709 QVEDDOLCKLYCTAEGDFFPSLSNKYKQDTPCESDSRNVICIDIGCRVGCNDVYLSDAV 768
DB 609 RGGGVKACSLTSLAEGNFYTERAAAVDGTPCRPDVIDICVSGECHKVACDRLGSDLR 668
QY 769 EDVCGVGNNGNSACTIRGLYTKHHTNOYHMTTISGARSTIRYMANVSTVYSRNA 828
DB 669 EDCKRCVCGSGSACETTEGVFSPASPGAAYBDVWIMIKSGVHIFIDLTNLSLHAKGD 728
QY 829 LRBYLNGHWTVDVPGRYKFSGTTFDYRRSYNEBENLITAGPTNETLIVELLFGSRNGV 888
```

```

DB 729 QESLLEGLPGTPQPHRLPLAGTTFOLROGPDQVOSLEALGPINASLIWVLTARTELPAL 788
QY 889 AMEYSMPRLGTEKQPPAQPSTYMAIVR-SBCSVSCGG 925
DB 789 RYRENP-IAEDSLP-----YSWHVAPWTKCSAQCAAG 821

RESULT 11
US-09-369-364A-13
; Sequence 13, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Aptec, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satochi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ. ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ. ID NO 13
; LENGTH: 1882
; TYPE: PRT
; ORGANISM: Homo sapiens ADAMTS-9
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (468)
; OTHER INFORMATION: Xaa = C
; NAME/KEY: MOD RES
; LOCATION: (521)
; OTHER INFORMATION: Xaa = Y
US-09-369-364A-13

Query Match      20.2%; Score 1056; DB 3; Length 1882;
Best Local Similarity 28.2%; Pred. No. 8.6e-85;
Matches 278; Conservative 142; Mismatches 315; Indels 252; Gaps 33;

QY 100 RMDDEAGNHRSOQTNTGNTGTLH-----VLQYDLSAENVDRGQVSHLMDHQ 151
DB 17 RDLAEMG--SPDAAAVRKDRLHPROVKLETLSEYELVSPRVALDBEPPTNV-HFK 72
QY 152 RRRRAV-----AVEVESLHLRLKGRPHDFMDLRTSSIVAPGFIVQTIG 197
DB 73 KTRRSINSATDPPAPASSSSSTSSQAHYKLSAFQOQFLNLTAAAGFTAPLPTTLG 132
QY 198 KTGTSKVQTLPPED---FCFY---QGSLSRH-RNSPSHGKFCGEGSTRTLKLNSQKC 248
DB 133 TPGVNTQKFYSBEAEALKHCFYRLCYOYLRAHGRHP-----LLRNEHK- 177
QY 249 PRDSVFPRAQCAENHSRRPRGHHYKMYKRYTOVEADLCKLYCTAEGDFFPSLSNVKDG 308
DB 178 -----NRHSDKKKTARMGGRINLAGVAALN----- 206
QY 309 TPCSEDSRNVICIDIGELSVSTSAAMPQPKEDFLTPDEYKSLRHRSLSRSHR-N 366
DB 207 -----SGLATEAFSAIGNKT-----NTRKKTTHRTKTRFLS 238
QY 367 BELNVEITLVVDKMMQNHENITTYVLTILNVSALFPGDGLMGK----- 412
DB 239 YPRFEVLVVADNRVSYHG-ENLQHYILTLMSIVASIYKDPISGILNIVNLIVIH 297
QY 413 -----DGRHDAHLILGDDTCMKNEPCDTLGFAPIS 445
DB 298 EDDPSISFNAQTLTNFCQWQHSNPPGGIHDTAVLLTRQDLCR-AHDKCDTLGAEIG 356
QY 446 GMSCKYRSCITINBDTGGLAFTIAHESGNPFGMIHDEGNMK-----KSEGNISPTLAG 501
DB 357 TIGDPTFRSCISISDSLSLSTAFTHLHGLIVFNNPHD-DNNKCEBVGKSPQYMAATLNF 415
QY 502 RNVGFSWSPCSROYLHKFLSTAQAICLADQPKPVKEYKYPEKLPGELYDANTQCKMQFGE 561
```

Db 416 YTPPMWMSKSRKTYTEFLDTGYGECLENEPES-RPYPLFVQLPGILYVNNKXELIFGP 474  
QY 562 KATLCMLDFPKDKCALMCHRIG---RKCETKMPAAEGTICGHDWMCRCGOCVKYDGR 618  
Db 475 GSGVCEPMMQ---CRRLMNNVNGVHGKCRTOHTPMADGTCEPBGKCKXGCVPEMVD 531  
QY 619 PKRTHHWSMSWSPCSTRCCGGVSHRSLCTNPKPSHGKFCESGTRTLKLCNSQKCP 678  
Db 532 P-VTDSWGSWSPGRTSCGIGITKALRECNRPFKNGKCYVARRMKFKSCNTEPCL 590  
QY 679 RDSVFPRAQCAENHNRFRGRHY-----KMKP-YTQVEDODLCKLYCIAEGPDEF 728  
Db 591 KQKRDTRDECA-----HFGKHFNINGLLPNRWPKYSGLIMKRCILFCVAAGTAY 645  
QY 729 FSLSNKYKOSTPCSESRNVCIDGICERVGCNDVLGSDAVEDVCGVCGNNSACTIHRL 788  
Db 646 YQLRDHVIDGTGCGODTNDICVQGLCRQAGCDHVLNSKARDKCKGCGGNSCKTVAQT 705  
QY 789 YTKGHHNTQYHNVTPSGARSLRIYEMNVS-----TSYISVNNALRRYYLNGHWVDM 843  
Db 706 FNTVHY--GNTVTVRLPAGATNIDVRQHSFSGETDDNYLALSSKGEFLNPNFVTVMA 763  
QY 844 GR-YKESGTFDYRRSYNEPENLIATGPTNETLIVELLFOGR--NPGVAMEYSMPRLGTE 900  
Db 764 KREIRGNMNVESGSEIATVERINSTDRIGELLQVLSVGLKYNPDVXSENIIP---IE 820  
QY 901 KQRP-----AOPSY----- 909  
Db 821 DKQCYVNNSHGPMQACSKPCQGERKRLVCTRESQDLTVSDQRCDRLPQPGHITPECGT 880  
QY 910 ----TWAIV-RSECSVSCG--GGRCLPV 930  
Db 881 GCDLRHNVASRSECSAQCGLGRTLDI 907  
RESULT 12  
US-09-321-987B-4  
/ Sequence 4, Application US/09321987B  
/ Patent No. 6730820  
/ GENERAL INFORMATION:  
/ APPLICANT: Kimble, Judith E  
/ APPLICANT: Belleloch, Robert H  
/ TITLE OF INVENTION: Agent and Method for Modulating Cell Migration  
/ FILE REFERENCE: 960296, 95386  
/ CURRENT APPLICATION NUMBER: US/09/321, 987B  
/ CURRENT FILING DATE: 1999-05-28  
/ PRIOR APPLICATION NUMBER: 60/087,170  
/ PRIOR FILING DATE: 1998-05-29  
/ PRIOR APPLICATION NUMBER: 60/129,023  
/ PRIOR FILING DATE: 1999-04-13  
/ NUMBER OF SEQ ID NOS: 5  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 4  
/ LENGTH: 950  
/ TYPE: PR  
/ ORGANISM: Murine  
US-09-321-987B-4  
Query Match 19.5%; Score 1022.5; DB 4; Length 950;  
Best Local Similarity 30.6%; Pred. No. 2,9e-82;  
Matches 26; Conservative 99; Mismatches 319; Indels 185; Gaps 32;  
QY 167 LRLKGRHDFHNDLRTSSSLVAPGFVQTLGKTGYSVOTLPED--FCFQGSIRSHR 223  
Db 64 LRLDAPGQQLHLKLDQDSGFLAPGFTLQTVGRSPGSEAOHLDPGTDLAHCFSYSGTVNGD- 122  
QY 224 NSPSSHGKFCESGSTRTLKLCNSQKCPRDSVDPRAAQCAENHNRFRGRHYKMKPYQVA 283  
Db 123 -----PGSAALSLCEG-----YKGFY----- 140  
QY 284 DLCKLYCIAEGPDEFPS-----LSNKYKDGTPCSEDSRN-----VCIDG 322  
Db 141 -----LQGEFFLQPARAVATERLAVAVPEESASAPQPHILARRRRSGGAKC--G 190

QY 323 ICELSVSTSAMPO-----PEKEDLFLPDEYKSLRHKSLSLRHNEELN 370  
Db 191 VMDDETLFTSDRPPSQUTRNQWVRADPTPODAG--KSPGSGIRKRFRV-----SSPRY 243  
QY 371 VETLVVVDKXMMQNNHENTITTYVLTILNVSALK----- 406  
Db 244 VETMLVADQSMADFHG--SGLKHYLLTLFSVAARFYKHPISIRNSISLVVKKILVIEEQKG 302  
QY 407 -----DGLMKDQTRDHAILLTGLDICSWMKEPCDTLGFAPIS 445  
Db 303 PEVTSNALLTLNFCNMQKHNSPSDRDREHYDTAILFTROLG--SHTCOTLGHADVG 360  
QY 446 GMSKYRSCSTINEDTGLAFTIAHSGHNFPMIHDEGNNCKKSEB-----NIMSPTLA 500  
Db 361 TVCDPSRSCSVIEDGLQAAFTTAHELGHVFMPHD--DAKHASLNGVTDGSHLWASMLS 419  
QY 501 GRNGVFSWSPCROYLHKFSLTAQALCLADQPKVXKYPKELRGELYDATPOCKMQG 560  
Db 420 SLDSQPMSPCSAYNVTSFLDNGHGECLMD--KPNPIKLPSDLPGTLVDANROCOFTFG 477  
QY 561 EKAKLCMLDFKKDICALMCHRIGRK-----CETKMPAAEGTICGHDWMCRCGOCVKYX 615  
Db 478 ESKKHC--PDAASTCTTLMC--TGTSGLIVCQTHGFPMADGTSCEGKMCVSGKCVNKT 533  
QY 616 D--EGPKPTHGMSWSSWSPCSTRCCGGVSHRSLCTNPKPSHGKFCESGTRTLKLCN 673  
Db 534 DMKHRTATPVHSGWGPWGCDSRTCCGGGVQYTMRECONPVKNGKCYCEGRVVRSCN 593  
QY 674 SOKCP-RDSVFPRAQCAEHN--SRFRGRH--YKMKP-YTQVEDODLCKLYCIAEGPDEF 727  
Db 594 IEDCDNNGKTFREQCAHNEFSASFGNEPTVMTPTKAGVSPDKRLCEKAGIGY 653  
QY 728 FSLSNKYKDGTPCSEDSRNVCIDGICERVGCNDVLGSDAVEDVCGVCGNNSACTIHRLG 787  
Db 654 FFLVLPKVVDTGCPGPDSTVCGQCVKAGCDRIIDKKKFKDKCGVGGANSTCKXMSG 713  
QY 788 LYTKGHHNTQYH-NVTPSGARSLRIYEMNV-----TSYISVNNALRRYYLNGHWVDM 841  
Db 714 IVTS---TRPGYHDIVTIPAGATNIEVGHNRQGRSRRNGSFLAIPAAQGYTLNPNFTLS 770  
QY 842 WGR-YKESGTFDYRRSYNEPENLIATGPTNETLIVELLFOGR--NPGVAMEYSMPRLG 898  
Db 771 TLEQULTYKGVLYKSGSALLERISPSPLKEPULTVOLVNGHALRPKIKFTYMKK-- 828  
QY 899 TEKOPPAQSYT-WAIVR-SRCSVSCGG 925  
Db 829 KTESFNALPTFSEWVIEEMGECSTCGSG 857  
RESULT 13  
US-09-981-953A-2  
/ Sequence 2, Application US/09981953A  
/ Patent No. 6689599  
/ GENERAL INFORMATION:  
/ APPLICANT: RACIE, LISA A.  
/ APPLICANT: TWINE, NATALIE C.  
/ APPLICANT: AGOSTINO, MICHAEL J.  
/ APPLICANT: WOLFMAN, NEIL  
/ APPLICANT: MORRIS, ELISABETH A.  
/ TITLE OF INVENTION: NOVEL AGGREGANSE MOLECULES  
/ FILE REFERENCE: 08702, 0075-00000  
/ CURRENT APPLICATION NUMBER: US/09/981, 953A  
/ CURRENT FILING DATE: 2001-10-18  
/ PRIOR APPLICATION NUMBER: 60/242,317  
/ PRIOR FILING DATE: 2000-10-20  
/ NUMBER OF SEQ ID NOS: 22  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 2  
/ LENGTH: 770  
/ TYPE: PR  
/ ORGANISM: Unknown Organism  
FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Amino acid  
OTHER INFORMATION: sequence of the aggreccanase molecule  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (200)  
OTHER INFORMATION: Any amino acid  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (214)  
OTHER INFORMATION: Any amino acid  
US-09-981-953a-2

Query Match 19.5%; Score 1022; DB 4; Length 770;  
Best Local Similarity 37.8%; Pred. No. 2.3e-82;  
Matches 213; Conservative 91; Mismatches 207; Indels 52; Gaps 16;

QY 379 KKKMOMH-GHEINTTYVLTILNMVSALEFKDLMGKOTRBDHAILLTGLDICSMMKPECD 437  
DB 41 QKSIVNHSQHGN-----ALPENGV-----ANHDTAVLTIRYDICIYKXKPCG 82  
QY 438 TLGAPARISGMSKYRSTINEDTGLAFTIAHSGHNPQMIDHSEGNMC---KSEGN1 494  
DB 83 TLGLAVGCMCEBERSSVVEDIGLAFRTIAHEIGTFPMNDGVNCSGAGQDPKAL 142  
QY 495 MSPTLAGRVGVSFMSPCSRQYLHKFLSTAQALCLADQPKPKVKKYPEKLPGLYDANTQ 554  
DB 143 MAHITMKTPFVWSSCRDYITSFLDSGPG-ALPEQPAPQTGLCVPDSDGTG---PSLR 197  
QY 555 CK-----WQPEBKALCMLDRKDOI CKALMCHRIKGRKCTETFMRAEETIC-GHDM-- 604  
DB 198 CRAMPPLSAW-----SQIASVXI-REVCSELWCLSKSNRITNSIPAAEGTILCQTHITDK 251  
QY 605 -MCRGGQCVVYGDGEPKPTGHMSDMSWSPSCRTCCGGVSHSRSLCTNPKPSHGKFCF 653  
DB 252 GNCYKRVCTPFGSR-PEGVDGANGPMTPMGDCSRCCGGVSSSSRCHDSRPTIGKRYCL 310  
QY 664 GSTRTILKLCNSQKCPDSDVDFRAQCAEHNSRRFRGHYKMKPYTOVEDDLCLYCIAE 723  
DB 311 GERRRHRSCTDIDCPGSDPQFREVQCSBFDSIPFRGKFXMKTY-RGGGVKACSLTCLAE 369  
QY 724 GPDFFPSLSKXVDGTPCSEDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCGNNSACT 753  
DB 370 GFNFYTERAAVAVDGTPCRDVTYDICSGBCKHVGCDRVLSDLRBDCKXVCGGDSACE 429  
QY 784 IHRGLTYKHHHTQYHMTTIPSGARSIRIYEMNVSTSYISVANALRRYYLNGHMTVDM 843  
DB 430 TIEGVSPASPGAGYEDVWIPKGSVAHIFIQDLNLSLHALKGDSLLBELPGTPQP 489  
QY 844 GRKFSGTTFDYRSYNPENLJATGPTNETLIVELLFQGRNPQVAMWEXSMPLRGTEKOP 903  
DB 490 HRLPLAGTTFQLRQGPQVQSLBALGPINSLIVMTLARTELPALRYRFAVAF-IARDSLP 548  
QY 904 PAQPSYTWALVR-SEGSVSCGG 925  
DB 549 P---YSMVAAPWTKCSAQACAG 567

RESULT 14  
US-09-369-364A-15  
Sequence 15, Application US/09369364A  
Patent No. 6391610  
GENERAL INFORMATION:  
APPLICANT: Apte, Suneel  
APPLICANT: Hurekainen, Tiina L.  
APPLICANT: Hirohata, Satoshi  
TITLE OF INVENTION: Nucleic Acid Encoding Zinc Metalloproteases  
FILE REFERENCE: 26473/4007/10-30-00  
CURRENT APPLICATION NUMBER: US/09/369,364A  
NUMBER OF SEQ ID NOS: 1999-08-06  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 874

TYPE: PRT  
ORGANISM: Mus musculus ADAMTS-9  
US-09-369-364A-15

Query Match 18.9%; Score 991; DB 3; Length 874;  
Best Local Similarity 34.2%; Pred. No. 1.7e-79;  
Matches 215; Conservative 107; Mismatches 210; Indels 96; Gaps 20;

QY 371 VETLVVVDKKMOMHGHENITTYVLTILNMVSALEFKDLMGK----- 412  
DB 134 VEVMTVADHRMTLYHG-ANLQHYILTLMSIIVASIVYDSSIGNLINIVYVNVIIHNEQBS 192  
QY 413 -----DGRDHAILLTGLDICSMMKPECDTGLAPARISGMC 448  
DB 193 PYINFAQTLLKNFCOMHSSKNVIGSIQHDVAVLTREDIR-AQKCPYTLGAEAGTIC 251  
QY 449 SKYRSTINEDTGLAFTIAHSGHNPQMIDHSEGNMC---KSEGN1MSTLAGRNG 504  
DB 252 DFRSCSISDSGLSTAFTHAHLGHVFNNMPHD-DSNCKCEGVKSPQHVMAFTLNPYTN 310  
QY 505 VFSWSPCSRQYLHKFLSTAQALCLADQPKPKVKKYPEKLPGLYDANTQCKMQFGKAK 564  
DB 311 PMMSKCSKRYTIFELDTGYGECLENPAS-RYPLPSQLPGLLYVNNQCELIIFPGSQ 369  
QY 565 LCMLEDFKDOI CKALMCHRIG---RKCEYFMRAEETICGHDMWCRGGQCVKYGDGEPK 621  
DB 370 VCPYMMQ---CRRLWCNNVDGAHKCKTQHTPMAQDTBCEBPKGKCFVPRMEGP-A 425  
QY 622 TGHMSDMSWSPSCRTCCGGVSHSRSLCTNPKPSHGKFCFCESTYTLKLCNSQKCPDSD 651  
DB 426 IDGSMGWSHFQTCSTCCGKIKTALRECNRPKPKGVGRMKFSCNTEPCMKOK 485  
QY 682 VDFRAQCAEHNSRRFRGRHY-----KMKP-YTOVEDDLCLYCIAEGDFEFSI 721  
DB 486 RDPREQCA-----HDKGHFNINGLBSVRMPFKYSGLIMDRCLFQVAVAGNTAYQL 540  
QY 732 SNKRVKGTCPSEDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCGNNSACTIHRGLYTK 791  
DB 541 RDRVIDGTFCQDQINDICVQGLCRQAGCDHILNSKVRKDKCIGGDNSSCKTVAGTFT 600  
QY 792 HHHTQYHMTTIPSGARSIRIYEMNV-----TSYISVANALRRYYLNGHMTVDM 845  
DB 601 VHY--GYNVTVRIPAGATSIDVRQHSFSSKSEDDNYLALNSNGEFLNGDFVNSKBE 658  
QY 846 YKFSGTTFDYRSYNPENLJATGPTNETLIVELLFQGR-NGVAMWEXSMPLRGTEKOP 903  
DB 659 VAVGSADVTSQSDNVCERLNTDRIEELILQVLSVGLYNPDVAYSFNIP---IEDKP 715  
QY 904 PAQPSY-----TWALVRSEGSVSCGG 926  
DB 716 --QQFYMSHGPPW-----QACSKPCQGER 737

RESULT 15  
US-09-130-491-2  
Sequence 2, Application US/09130491  
Patent No. 6416974  
GENERAL INFORMATION:  
APPLICANT: Holtzman, Douglas A.  
APPLICANT: Gooderl, Andrew D.J.  
TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83  
FILE REFERENCE: 09404/041001  
CURRENT APPLICATION NUMBER: US/09/130,491  
CURRENT FILING DATE: 1998-08-07  
EARLIER APPLICATION NUMBER: US 60/058,108  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: US 60/054,961  
EARLIER FILING DATE: 1997-08-06  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 967  
TYPE: PRT



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using BW model

Run on: September 9, 2005, 21:47:39 ; Search time 1301 Seconds  
(without alignments)  
288.623 Million cell updates/sec

Title: US-09-981-151D-8

Perfect score: 5236  
Sequence: 1 MKPRARGWGLALMWLLAQ.....LEAACPSATAYIALAFLES 952

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1777461 seqs, 394431504 residues

Total number of hits satisfying chosen parameters: 1777461

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: Published Applications\_AA.\*  
2: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/2/pubppaa/PCT\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep.\*  
5: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/2/pubppaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubppaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubppaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubppaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubppaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubppaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubppaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubppaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubppaa/US10E\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/2/pubppaa/US10\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubppaa/US11\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/2/pubppaa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5236	100.0	952	US-09-981-151A-8	Sequence 8, Appli
2	5110	97.6	986	US-09-981-151A-2	Sequence 2, Appli
3	4103.5	78.4	791	US-09-981-151A-4	Sequence 4, Appli
4	3858.5	73.7	1224	US-10-275-107-51	Sequence 51, Appli
5	3846.5	73.5	1224	US-10-217-774-4	Sequence 4, Appli
6	3846.5	73.5	1224	US-10-296-616-2	Sequence 2, Appli
7	3846.5	73.5	1224	US-10-804-457-4	Sequence 4, Appli
8	3365	64.3	856	US-09-981-151A-6	Sequence 6, Appli
9	3286	62.8	1236	US-10-399-645-4	Sequence 4, Appli
10	2435.5	46.5	1221	US-10-240-545A-2	Sequence 2, Appli
11	2434.5	46.5	1082	US-10-363-937-17	Sequence 17, Appli

12	2434.5	46.5	1221	US-10-354-983-2	Sequence 2, Appli
13	2430	46.4	1375	US-10-120-801-48	Sequence 48, Appli
14	2411.5	46.1	1071	US-10-354-983-4	Sequence 4, Appli
15	2408	46.0	1081	US-10-120-801-46	Sequence 46, Appli
16	2408	46.0	1081	US-10-391-364-87	Sequence 87, Appli
17	2364	45.1	1162	US-10-161-493-124	Sequence 124, App
18	2265	43.3	862	US-10-226-560-2	Sequence 2, Appli
19	2265	43.3	862	US-10-990-935-2	Sequence 2, Appli
20	2255	43.1	914	US-10-188-186-132	Sequence 132, App
21	2247.5	42.9	919	US-10-188-186-130	Sequence 130, App
22	2196.5	41.9	934	US-10-275-107-53	Sequence 53, Appli
23	2079.5	39.7	1123	US-10-120-801-45	Sequence 45, Appli
24	1559	29.8	661	US-10-354-983-8	Sequence 8, Appli
25	1543.5	29.5	491	US-10-217-774-2	Sequence 2, Appli
26	1543.5	29.5	491	US-10-804-457-2	Sequence 2, Appli
27	1391	26.6	959	US-09-788-043C-1	Sequence 1, Appli
28	1380	26.5	908	US-09-963-791-2	Sequence 2, Appli
29	1380	26.5	908	US-10-419-276-2	Sequence 2, Appli
30	1380	26.5	908	US-11-027-743-2	Sequence 2, Appli
31	1380.5	26.4	1120	US-10-467-042-6	Sequence 6, Appli
32	1380.5	26.4	1120	US-11-046-868-6	Sequence 6, Appli
33	1376	26.3	684	US-10-103-377C-2	Sequence 2, Appli
34	1342	25.6	353	US-10-161-493-130	Sequence 130, App
35	1342	25.6	353	US-10-161-493-134	Sequence 134, App
36	1339	25.6	353	US-10-161-493-128	Sequence 128, App
37	1332	25.4	349	US-10-161-493-126	Sequence 126, App
38	1332	25.4	353	US-10-161-493-132	Sequence 132, App
39	1319	25.2	757	US-09-963-791-24	Sequence 24, Appli
40	1319	25.2	757	US-10-419-276-24	Sequence 24, Appli
41	1319	25.2	757	US-11-027-743-24	Sequence 24, Appli
42	1257	24.0	1590	US-09-788-043C-5	Sequence 5, Appli
43	1246	23.8	1866	US-10-386-414-2	Sequence 2, Appli
44	1243	23.7	1044	US-09-858-081-9	Sequence 9, Appli
45	1242	23.7	1103	US-10-275-107-50	Sequence 50, Appli

ALIGNMENTS

RESULT 1  
US-09-981-151A-8  
; Sequence 8, Application US/09981151A  
; Publication No. US20030212256A1  
; GENERAL INFORMATION:  
; APPLICANT: Edinger, Shlomit R  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: MacDougall, John R  
; APPLICANT: Malyankar, Murtel M  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Peyman, John A  
; APPLICANT: Stone, David J  
; APPLICANT: Gunther, Erik  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Shimkets, Richard A  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Paturajan, Meera  
; APPLICANT: Taupier Jr, Raymond J  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Zehrusen, Bryan D  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Gargolli, Esha A  
; APPLICANT: Fernandes, Elma R  
; APPLICANT: Gorman, Linda  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-168  
; CURRENT APPLICATION NUMBER: US/09/981,151A  
; PRIOR FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 60/241,040  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/241,058



1 PRIOR FILING DATE: 2000-10-17  
1 PRIOR APPLICATION NUMBER: 60/241,063  
1 PRIOR FILING DATE: 2000-10-17  
1 PRIOR APPLICATION NUMBER: 60/241,243  
1 PRIOR FILING DATE: 2000-10-17  
1 PRIOR APPLICATION NUMBER: 60/242,152  
1 PRIOR FILING DATE: 2000-10-20  
1 PRIOR APPLICATION NUMBER: 60/242,482  
1 PRIOR FILING DATE: 2000-10-23  
1 PRIOR APPLICATION NUMBER: 60/242,611  
1 PRIOR FILING DATE: 2000-10-23  
1 PRIOR APPLICATION NUMBER: 60/242,612  
1 PRIOR FILING DATE: 2000-10-23  
1 PRIOR APPLICATION NUMBER: 60/242,880  
1 PRIOR FILING DATE: 2000-10-24  
1 PRIOR APPLICATION NUMBER: 60/242,881  
1 PRIOR FILING DATE: 2000-10-24  
1 Remaining Prior Application data removed - See file wrapper or PALM.  
1 NUMBER OF SEQ ID NOS: 160  
1 SOFTWARE: PatentIn Ver. 2.1  
1 SEQ ID NO 8  
1 LENGTH: 952  
1 TYPE: PRT  
1 ORGANISM: Homo sapiens  
US-09-981-151A-8

Query Match 100.0%; Score 5236; DB 10; Length 952;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 952; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MKPRAGMGLALMLLQVAVQVPSGRSHQGNNGSGOLESPRLISRGRRRLTAMS 60  
1 MKPRAGMGLALMLLQVAVQVPSGRSHQGNNGSGOLESPRLISRGRRRLTAMS 60  
61 PLFSACTCVRHGTRSSGASMEPERPASSSTRGAAGLDGKRDMDAGNHSQQTNTGTENO 120  
61 PLFSACTCVRHGTRSSGASMEPERPASSSTRGAAGLDGKRDMDAGNHSQQTNTGTENO 120  
121 TLHVLTYQVLVSAYEYDRHGDYVSHIEMHQRRAVAVSEVSLHLRLKGRPHDFHML 180  
121 TLHVLTYQVLVSAYEYDRHGDYVSHIEMHQRRAVAVSEVSLHLRLKGRPHDFHML 180  
181 RTSSSLVAGPFIQTLGKTGTSVOTLPEDPCFYGSLRSHRNSPHGKCEGSTRTL 240  
181 RTSSSLVAGPFIQTLGKTGTSVOTLPEDPCFYGSLRSHRNSPHGKCEGSTRTL 240  
181 RTSSSLVAGPFIQTLGKTGTSVOTLPEDPCFYGSLRSHRNSPHGKCEGSTRTL 240  
241 KLCNSQKCPRDSVDFRAACAEHNSRRFRGRHYKMKPYTQVEADLCKLCLAEGRDFEFS 300  
241 KLCNSQKCPRDSVDFRAACAEHNSRRFRGRHYKMKPYTQVEADLCKLCLAEGRDFEFS 300  
301 LSNKYVDGTPCSEDSRNVCIIDGICELSVYSTAHMPQPKEDLFIIPDEYKSCLAHRKSL 360  
301 LSNKYVDGTPCSEDSRNVCIIDGICELSVYSTAHMPQPKEDLFIIPDEYKSCLAHRKSL 360  
361 LASHREBELNVELTVVDDKKMMQNHENITTVTLILMWSALFKDGLMGXGDRHDA 420  
361 LASHREBELNVELTVVDDKKMMQNHENITTVTLILMWSALFKDGLMGXGDRHDA 420  
421 ILTGLDICSWMNEPCDTLGFAPISGMSKYSCTINEDTGLGLAFTIAHSGHNFMTI 480  
421 ILTGLDICSWMNEPCDTLGFAPISGMSKYSCTINEDTGLGLAFTIAHSGHNFMTI 480  
481 DEEGNCKSEBENISPTLAGRNGVSSAPCSROYLHKLSTAOAICLADQPKPYEYKY 540  
481 DEEGNCKSEBENISPTLAGRNGVSSAPCSROYLHKLSTAOAICLADQPKPYEYKY 540  
541 PEKLPGELVDANTQCKMOPGEKAKLCMLPFKKDICALMCHNIGRCETKMPAAEGTIC 600  
541 PEKLPGELVDANTQCKMOPGEKAKLCMLPFKKDICALMCHNIGRCETKMPAAEGTIC 600  
601 GHDMCRGGQCVKYGDGEPKPTHGHMSDWSWSPCSRTCGGVSRSRLCTNPKPSHGK 660  
601 GHDMCRGGQCVKYGDGEPKPTHGHMSDWSWSPCSRTCGGVSRSRLCTNPKPSHGK 660

661 FCEGSTRTLKLCNSQKCPRDSVDFRAACAEHNSRRFRGRHYKMKPYTQVEDQDLCIKYC 720  
661 FCEGSTRTLKLCNSQKCPRDSVDFRAACAEHNSRRFRGRHYKMKPYTQVEDQDLCIKYC 720  
721 IAEGRDFEFSLSNKKYDGTCPSEDSRNVCIIDGICERVCGDNVLGSDAEDVCGVCGNNS 780  
721 IAEGRDFEFSLSNKKYDGTCPSEDSRNVCIIDGICERVCGDNVLGSDAEDVCGVCGNNS 780  
781 ACTIRHGLYTKHHNTQYHHMTWIPSGARSIRIYEMNSTSYISVRNALRRYLLNGHWT 840  
781 ACTIRHGLYTKHHNTQYHHMTWIPSGARSIRIYEMNSTSYISVRNALRRYLLNGHWT 840  
841 DMPGRYKSGTTFEDYRISYNEPENIATGPTNETLIVELLFOGRNPGVAMEYSMPRLGTE 900  
841 DMPGRYKSGTTFEDYRISYNEPENIATGPTNETLIVELLFOGRNPGVAMEYSMPRLGTE 900  
901 KOPRQOPQYTAIVRSECSVSCGGRCPLVLLLEAACQPSATAYIALAFLES 952  
901 KOPRQOPQYTAIVRSECSVSCGGRCPLVLLLEAACQPSATAYIALAFLES 952

RESULT 2  
US-09-981-151A-2  
1 Sequence 2, Application US/09981151A  
1 Publication No. US20030212256A1  
1 GENERAL INFORMATION:  
1 APPLICANT: Edinger, Shlomit R  
1 APPLICANT: Gerlach, Valerie  
1 APPLICANT: MacDougall, John R  
1 APPLICANT: Maljankar, Muriel M  
1 APPLICANT: Smithson, Glenda  
1 APPLICANT: Millet, Isabelle  
1 APPLICANT: Peyman, John A  
1 APPLICANT: Stone, David J  
1 APPLICANT: Gunther, Erik  
1 APPLICANT: Ellerman, Karen  
1 APPLICANT: Shimkeles, Richard A  
1 APPLICANT: Padigaru, Muralidhara  
1 APPLICANT: Guo, Xiaojia  
1 APPLICANT: Paturajan, Meera  
1 APPLICANT: Taupier Jr, Raymond J  
1 APPLICANT: Burgess, Catherine E  
1 APPLICANT: Zernusen, Bryan D  
1 APPLICANT: Kekuda, Ramesh  
1 APPLICANT: Spytek, Kimberly A  
1 APPLICANT: Gangolli, Esna A  
1 APPLICANT: Fernandes, Elma R  
1 APPLICANT: Gorman, Linda  
1 TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
1 FILE REFERENCE: 21402-168  
1 CURRENT APPLICATION NUMBER: US/09/981,151A  
1 PRIOR FILING DATE: 2001-10-16  
1 PRIOR APPLICATION NUMBER: 60/241,040  
1 PRIOR FILING DATE: 2000-10-17  
1 PRIOR APPLICATION NUMBER: 60/241,058  
1 PRIOR FILING DATE: 2000-10-17  
1 PRIOR APPLICATION NUMBER: 60/241,063  
1 PRIOR FILING DATE: 2000-10-17  
1 PRIOR APPLICATION NUMBER: 60/241,243  
1 PRIOR FILING DATE: 2000-10-17  
1 PRIOR APPLICATION NUMBER: 60/242,152  
1 PRIOR FILING DATE: 2000-10-20  
1 PRIOR APPLICATION NUMBER: 60/242,482  
1 PRIOR FILING DATE: 2000-10-23  
1 PRIOR APPLICATION NUMBER: 60/242,611  
1 PRIOR FILING DATE: 2000-10-23  
1 PRIOR APPLICATION NUMBER: 60/242,612  
1 PRIOR FILING DATE: 2000-10-23  
1 PRIOR APPLICATION NUMBER: 60/242,880  
1 PRIOR FILING DATE: 2000-10-24  
1 PRIOR APPLICATION NUMBER: 60/242,881  
1 PRIOR FILING DATE: 2000-10-24

Remaining Prior Application data removed - See File Wrapper or PALM.  
/ NUMBER OF SEQ ID NOS: 160  
/ SOFTWARE: Patent In Ver. 2.1  
/ SEQ ID NO 2  
/ LENGTH: 986  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: VARIANT  
/ LOCATION: (283)  
/ OTHER INFORMATION: wherein Xaa is any amino acid.  
/ NAME/KEY: VARIANT  
/ LOCATION: (792)  
/ OTHER INFORMATION: wherein Xaa is any amino acid.  
US-09-981-151A-2

Query Match 97.6%; Score 5110; DB 10; Length 986;  
Best Local Similarity 94.6%; Pred. No. 0;  
Matches 940; Conservative 1; Mismatches 3; Indels 50; Gaps 4;

QY 1 MKPRAGMRLALMLLAQVAOVSGRSHORNGRSGQLASPPRLSRGPRRLTAMS 60  
DB 1 MKPRAGMRLALMLLAQVAOVSGRSHORNGRSGQLASPPRLSRGPRRLTAMS 60  
QY 61 PLPSAGTCVAGHGRSGSAMERPERPASSSTRGAAGLDGKGRMDAGNHRSGQTNTGTENG 120  
DB 61 PLPSAGTCVAGHGRSGSAMERPERPASSSTRGAAGLDGKGRMDAGNHRSGQTNTGTENG 120  
QY 121 TLHLVLTQYDLSAIEVDHGRDYSHEIMHRRRAVAASEVSLHLRLKGRPHDPMDL 180  
DB 121 TLHLVLTQYDLSAIEVDHGRDYSHEIMHRRRAVAASEVSLHLRLKGRPHDPMDL 180  
QY 181 RTSSSLVABPFIYQTGKTGKTVQTLPRPDPFCYQSLASHNSPHGKPFEGSTRLL 240  
DB 181 RTSSSLVABPFIYQTGKTGKTVQTLPRPDPFCYQSLASHNSPHGKPFEGSTRLL 240  
QY 181 RTSSSLVABPFIYQTGKTGKTVQTLPRPDPFCYQSLASHNSPHGKPFEGSTRLL 240  
DB 181 RTSSSLVABPFIYQTGKTGKTVQTLPRPDPFCYQSLASHNSPHGKPFEGSTRLL 240  
QY 241 KLCNSQKCPRSDVDFRAQCAEHNSRRFRGRHYKMKPYTOVEADLCYLCTIAGGFDFFS 300  
DB 241 KLCNSQKCPRSDVDFRAQCAEHNSRRFRGRHYKMKPYTOVEADLCYLCTIAGGFDFFS 300  
QY 301 LSNKVKDGTFCSEDSRNVICIDGICELSVSTSAHMPQPPKEDFILPDEYKSCLRHRS 360  
DB 301 LSNKVKDGTFCSEDSRNVICIDGICELSVSTSAHMPQPPKEDFILPDEYKSCLRHRS 360  
QY 361 LBSHRBEELNVELTVVDDKMMQNHGENTTYVLTILNVLSALFKDGTIGGINIAIVG 420  
DB 361 LBSHRBEELNVELTVVDDKMMQNHGENTTYVLTILNVLSALFKDGTIGGINIAIVG 420  
QY 408 -----GLMGKDGTRHDHAILTLGLDICSWKNEPCDT 438  
DB 408 -----GLMGKDGTRHDHAILTLGLDICSWKNEPCDT 438  
QY 421 LILLEDQEPGLVSHADHTLSSFQCMQSGLMGKDGTRHDHAILTLGLDICSWKNEPCDT 480  
DB 421 LILLEDQEPGLVSHADHTLSSFQCMQSGLMGKDGTRHDHAILTLGLDICSWKNEPCDT 480  
QY 439 LGFAPISGMCKSKYRSCCTINEDTGLGLAFTIAHSGNFMHIDEGNMCKSEGNIMSPT 498  
DB 439 LGFAPISGMCKSKYRSCCTINEDTGLGLAFTIAHSGNFMHIDEGNMCKSEGNIMSPT 498  
QY 481 LGFAPISGMCKSKYRSCCTINEDTGLGLAFTIAHSGNFMHIDEGNMCKSEGNIMSPT 540  
DB 481 LGFAPISGMCKSKYRSCCTINEDTGLGLAFTIAHSGNFMHIDEGNMCKSEGNIMSPT 540  
QY 499 LAGRNVEFSGSPCSROYLHKFTLSTAOICLADQPKPKYKPEBKLPGLIYDANTQCKWQ 558  
DB 499 LAGRNVEFSGSPCSROYLHKFTLSTAOICLADQPKPKYKPEBKLPGLIYDANTQCKWQ 558  
QY 541 LAGRNVEFSGSPCSROYLHKFTLSTAOICLADQPKPKYKPEBKLPGLIYDANTQCKWQ 600  
DB 541 LAGRNVEFSGSPCSROYLHKFTLSTAOICLADQPKPKYKPEBKLPGLIYDANTQCKWQ 600  
QY 559 FGEKAKLCMLDFFKDDICKALMCHRIGRKCEKTFMPAEGTICGHDMWCRGGQCVKYGDEG 618  
DB 559 FGEKAKLCMLDFFKDDICKALMCHRIGRKCEKTFMPAEGTICGHDMWCRGGQCVKYGDEG 618  
QY 601 FGEKAKLCMLDFFKDDICKALMCHRIGRKCEKTFMPAEGTICGHDMWCRGGQCVKYGDEG 660  
DB 601 FGEKAKLCMLDFFKDDICKALMCHRIGRKCEKTFMPAEGTICGHDMWCRGGQCVKYGDEG 660  
QY 619 PKPTHGMSWMSWSPCSRTCGGVSHRSLCTNPXKSHGKFCESGTRTLKLCNSQKCP 678  
DB 619 PKPTHGMSWMSWSPCSRTCGGVSHRSLCTNPXKSHGKFCESGTRTLKLCNSQKCP 678  
QY 661 PKPTHGMSWMSWSPCSRTCGGVSHRSLCTNPXKSHGKFCESGTRTLKLCNSQKCP 720  
DB 661 PKPTHGMSWMSWSPCSRTCGGVSHRSLCTNPXKSHGKFCESGTRTLKLCNSQKCP 720  
QY 679 RDSVDFRAAACAEHNSRRFRGRHYKMKPYTOVEADLCYLCTIAGGFDFFSLSNKYKDG 738  
DB 679 RDSVDFRAAACAEHNSRRFRGRHYKMKPYTOVEADLCYLCTIAGGFDFFSLSNKYKDG 738  
QY 721 RDSVDFRAAACAEHNSRRFRGRHYKMKP-----QDCLKLYCTIAGGFDFFSLSNKYKDG 774  
DB 721 RDSVDFRAAACAEHNSRRFRGRHYKMKP-----QDCLKLYCTIAGGFDFFSLSNKYKDG 774

QY 739 TPCESDSRNVICIDGICERVCQNVIGSDAIVEDYGVCGNNGNSACTIHRGLYTKHHHTNQY 798  
DB 775 TPCESDSRNVICIDGICE-XGCDNVIGSDAIVEDYGVCGNNGNSACTIHRGLYTKHHHTN-H 832  
QY 799 YHAWTIPSGARSIRIEMNVSTSYISVRNALRRYYLNGHWTUMPRRYKFSCTTPDYRRS 858  
DB 833 YHAWTIPSGARSIRIEMNVSTSYISVRNALRRYYLNGHWTUMPRRYKFSCTTPDYRRS 892  
QY 859 YNEPENLIATGPTNETLIYELLFOGRNPGVAMEYSMPRLGTEKQPPAOPSYTMAIVRSEC 918  
DB 893 YNEPENLIATGPTNETLIYELLFOGRNPGVAMEYSMPRLGTEKQPPAOPSYTMAIVRSEC 952  
QY 919 SVSCGGRCCLPVLLLEAACQPSATAYIALAFLES 952  
DB 953 SVSCGGRCCLPVLLLEAACQPSATAYIALAFLES 986

RESULT 3  
US-09-981-151A-4  
/ Sequence 4, Application US/09981151A  
/ Publication No. US2003021256A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Edinger, Shlomit R  
/ APPLICANT: Gerlach, Valerie  
/ APPLICANT: MacDougall, John R  
/ APPLICANT: Malyanar, Muriel M  
/ APPLICANT: Smithson, Glenda  
/ APPLICANT: Millet, Isabelle  
/ APPLICANT: Pezman, John A  
/ APPLICANT: Stone, David J  
/ APPLICANT: Gunther, Erik  
/ APPLICANT: Ellerman, Karen  
/ APPLICANT: Shinkets, Richard A  
/ APPLICANT: Padigaru, Muralidhara  
/ APPLICANT: Guo, Xisaojie  
/ APPLICANT: Patlurajan, Meera  
/ APPLICANT: Taupier Jr, Raymond J  
/ APPLICANT: Burgess, Catherine E  
/ APPLICANT: Zerhusen, Bryan D  
/ APPLICANT: Kekuda, Ramesh  
/ APPLICANT: Spytek, Kimberly A  
/ APPLICANT: Gangolli, Esna A  
/ APPLICANT: Fernandes, Elma R  
/ APPLICANT: German, Linda  
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
/ FILE REFERENCE: 21402-168  
/ CURRENT APPLICATION NUMBER: US/09/981,151A  
/ PRIOR APPLICATION NUMBER: 60/241,040  
/ PRIOR FILING DATE: 2001-10-16  
/ PRIOR FILING DATE: 2000-10-17  
/ PRIOR APPLICATION NUMBER: 60/241,058  
/ PRIOR FILING DATE: 2000-10-17  
/ PRIOR APPLICATION NUMBER: 60/241,063  
/ PRIOR FILING DATE: 2000-10-17  
/ PRIOR APPLICATION NUMBER: 60/241,243  
/ PRIOR FILING DATE: 2000-10-17  
/ PRIOR APPLICATION NUMBER: 60/242,152  
/ PRIOR FILING DATE: 2000-10-20  
/ PRIOR APPLICATION NUMBER: 60/242,482  
/ PRIOR FILING DATE: 2000-10-23  
/ PRIOR APPLICATION NUMBER: 60/242,611  
/ PRIOR FILING DATE: 2000-10-23  
/ PRIOR APPLICATION NUMBER: 60/242,612  
/ PRIOR FILING DATE: 2000-10-23  
/ PRIOR APPLICATION NUMBER: 60/242,880  
/ PRIOR FILING DATE: 2000-10-24  
/ PRIOR APPLICATION NUMBER: 60/242,881  
/ PRIOR FILING DATE: 2000-10-24  
/ Remaining Prior Application data removed - See File Wrapper or PALM.  
/ NUMBER OF SEQ ID NOS: 160  
/ SOFTWARE: Patent In Ver. 2.1  
/ SEQ ID NO 4  
/ LENGTH: 791

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-981-151A-4

```

Query Match	Score	DB	Length
78.4%	4103.5	10	791

[illegible]

```

RESULT 4
US-10-275-107-51
? Sequence 51, Application US/10275107
? Publication No. US20040063107A1
? GENERAL INFORMATION:
? APPLICANT: PLOWMAN, GREGORY D.
? APPLICANT: WHITE, DAVID
? APPLICANT: SUDARSANAM, SUCHA
? APPLICANT: MANNING, GERARD
? APPLICANT: CAENEPEEL, SEAN R.
? APPLICANT: PAYNE, VILLA
? TITLE OF INVENTION: NOVEL PROTEASES
? FILE REFERENCE: 038602/1479
? CURRENT APPLICATION NUMBER: US/10/275,107
? CURRENT FILING DATE: 2003-11-03
? PRIOR APPLICATION NUMBER: PCT/US01/14431
? PRIOR FILING DATE: 2001-05-04
? PRIOR APPLICATION NUMBER: 60/201,879
? PRIOR FILING DATE: 2000-05-04
? NUMBER OF SEQ ID NOS: 105
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 51
? LENGTH: 1224
? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-275-107-51

```

Query Match	Score	DB	Length
73.7%	3858.5	DB 15	Length 1224

QY	1	МКРРАСМРГЛАЛМЛЛАОВАОВСРГШОСНГСОСЛЕАСРЛЛСРГРЛЛТАМС	60
Db	1	МКРРАСМРГЛАЛМЛЛАОВАОВАР-----АСМГ	31
QY	61	РЛФСАСТСВННГТРССАМЕРРРАСССТРГААЛДКСГДМДЕАГНННСОQТНТГЕНОQ	120
Db	32	РАААА-----РГСРВРРРРРРАЕРРГ-----ММКСГ-----	58
QY	121	ТЛМЛТОУДЛСАЕУВДННДРДУУШЕЛМНОРРРАВАЕУСЛНЛРЛГРННДРМДЛ	180
Db	59	-----БДУДСАЕУВДННДРДУУШЕЛМНОРРРАВАЕУСЛНЛРЛГРННДРМДЛ	112
QY	181	РТССЛВАРРФИУОЛГКГТКСУОТЛРРЕРФСЮОСЛШННСПНГКСРСЕТРЛ	240
Db	113	РТССЛВАРРФИУОЛГКГТКСУОТЛРРЕРФСЮОСЛШННСПНГКСРСЕТРЛ	171
QY	241	КЛСНСОКСРРДСВДРРАОСАЕННСРРРР-----НУККРПТУОВА-ДЛСКУС	291
Db	172	Р-----ТЕАДУРЛРЛРЛРЛШЛСМДЛ-ГРАОССРШВЛКРСТЕРПАРАСЕВЛТ	222
QY	292	АЕГДФЕФС--ЛСНКУАДГРРСЕБДСРНУСДІСЕЛСВУСТАННОРРЕДЛФИРДЕ	349
Db	223	СРМЕЛАННОРЛННСДЛРЛГР--ОКОНЕ-----ГРККМНОРРЕДЛФИРДЕ	270
QY	350	УКССЛННКСЛШННРЕБЛНВТЛЛВУДКММОННЕНІТТУУЛТЛМНВАЛРД--	407
Db	271	УКССЛННКСЛШННРЕБЛНВТЛЛВУДКММОННЕНІТТУУЛТЛМНВАЛРД	330
QY	408	-----ГМКСОГТРДННЛЛЛТГД	427
Db	331	ІГГНІНАІАУГЛЛЛЕДНОРГУІШННДНТЛСРСОМОСГМКОТТРДННЛЛЛТГД	390
QY	428	ІСМКОБЕСДТЛГАРІСМКСКІРССТІНЕТГЛГАЛТАІНЕСГННМІДБСГНМ	487
Db	391	ІСМКОБЕСДТЛГАРІСМКСКІРССТІНЕТГЛГАЛТАІНЕСГННМІДБСГНМ	450
QY	488	ККСЕГНІМСПТЛАГРНГВФСРПССОУЛННКТСТАОІСЛАОРПВККРПЕКЛР	547
Db	451	ККСЕГНІМСПТЛАГРНГВФСРПССОУЛННКТСТАОІСЛАОРПВККРПЕКЛР	510
QY	548	ЛДАНТЮСКОФЕКАКЛМДРКДІОСЛАМДНІРІГРКЕТКРМРАБЕГТІСГДММ	607





Db 571 GGCGVCKGDEGEPRTYGHMSDMSWSPCSTRCCGGVSHSRSLCTNPKPSHGKFCGSTR 630  
Qy 668 TLKLCNSQKCPRSDVDFRAAQCAEHNSRRRFRGHYKMKPYQVEDDCLCYCIAEGFDF 727  
Db 631 TLKLCNSQKCPRSDVDFRAAQCAEHNSRRRFRGHYKMKPYQVEDDCLCYCIAEGFDF 650  
Qy 728 FFSLSKRVKXGDTFPCSEDSRNVCTDGCERVGCNVLGSDAVEDVCGVCGNNSACTIHNG 787  
Db 691 FFSLSKRVKXGDTFPCSEDSRNVCTDGCERVGCNVLGSDAVEDVCGVCGNNSACTIHNG 750  
Qy 788 LTKKHHTTQYVMWVTPSGARSIRIYEMNVSTSYISVNAALRRYYLNGHMTWDMGRYK 847  
Db 751 LTKKHHTTQYVMWVTPSGARSIRIYEMNVSTSYISVNAALRRYYLNGHMTWDMGRYK 810  
Qy 848 FSGTTFDYRSYNEPNLITATGPTNETLIVELLFOGRNPGVAMEYMPRLGTEKOPAP 907  
Db 811 FSGTTFDYRSYNEPNLITATGPTNETLIVELLFOGRNPGVAMEYMPRLGTEKOPAP 870  
Qy 908 SYTWAIVRSECVSVCGGGR 926  
Db 871 SYTWAIVRSECVSVCGGGQ 889

RESULT 8  
US-09-981-151A-6  
Sequence 6, Application US/09981151A  
Publication No. US2003021256A1  
GENERAL INFORMATION:  
APPLICANT: Edinger, Shlomit R  
APPLICANT: Gerlach, Valerie  
APPLICANT: MacDougall, John R  
APPLICANT: Malyankar, Muriel M  
APPLICANT: Smithson, Glenda  
APPLICANT: Millet, Isabelle  
APPLICANT: Beyman, John A  
APPLICANT: Stone, David J  
APPLICANT: Gunther, Erik  
APPLICANT: Ellerman, Karen  
APPLICANT: Shlimes, Richard A  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Guo, Xiaojia  
APPLICANT: Patlurajan, Weera  
APPLICANT: Taupier Jr, Raymond J  
APPLICANT: Burgess, Catherine E  
APPLICANT: Zerhusen, Bryan D  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Spytek, Kimberly A  
APPLICANT: Gangoli, Beba A  
APPLICANT: Fernandes, Elma R  
APPLICANT: Gorman, Linda  
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-168  
CURRENT APPLICATION NUMBER: US/09/981,151A  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 60/241,040  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,058  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,063  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,243  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/242,152  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/242,482  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,611  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,612  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,880  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/242,881

Qy 129 DLVSAYEVHRDQDYSHETMHQRRRAVAVESESLHRLKGPBPHDMDLRTSSSLVA 188  
Db 19 DLVSAYEVHRDQDYSHETMHQRRRAVAVESESLHRLKGPBPHDMDLRTSSSLVA 75  
Qy 189 ---PGFT-----VOTLAKTGKTSYVTLPPBD----FCFYQ-GSLRS 221  
Db 76 NSQPGFLNLSNVSRSHWRQHASKRITTNAMLGESALASTRKANCVFLSFYFGSGMIRT 135  
Qy 222 H-----RNSPSH-----GKFCGGS-----TRTLKLCNSQKCPRSDVDFRA 257  
Db 136 BEADYFLRPLPSHLNKLGRAAQSSPSHYLYKREVLVTSRTWELAHQ---PLHSSDLRL 192  
Qy 258 AQAENHSRRFRGRHYKMKPYQVEADCLCYCIAEGFDFPFSLSKRVKXGDTFPCSEDSRN 317  
Db 193 GL---FQKHFGCRKK----- 206  
Qy 318 VCIDIGCELSVSTSAHMPDPKEDLFLPDEYKCLRHKSLRSHNEBLNVTLLVVV 377  
Db 207 -----YMPKPKEDLFLPDEYKCLRHKSLRSHNEBLNVTLLVVV 250  
Qy 378 DKMMQNHENITTVVTLIMVSLPFD----- 407  
Db 251 DKMMQNHENITTVVTLIMVSLPFDGTTGGININIAVGLILLEDEQGLVISHA 310  
Qy 408 -----GLMKDGTGRDHAILTGLDICSWKNEPCDTLGPAPISGMSKYSRCT 455  
Db 311 DHTLSFCOMQGLMKDGTGRDHAILTGLDICSWKNEPCDTLGPAPISGMSKYSRCT 370  
Qy 456 INEDTGLAFTIAHESGNFMHDEGNMCKSEBNMSTPLAGRNQVFSWSPSCROY 515  
Db 371 INEDTGLAFTIAHESGNFMHDEGNMCKSEBNMSTPLAGRNQVFSWSPSCROY 430  
Qy 516 LHKFLSTAQALCLADQPKVYKYPKLPGLYDANTQCKQOFGKALCHLDFKDLIC 575  
Db 431 LHKFLSTAQALCLADQPKVYKYPKLPGLYDANTQCKQOFGKALCHLDFKDLIC 490  
Qy 576 KALMCHIRKCEKTPMPAAEGTICGHDWCRGGQCVKYGDBGPKPTHGMSDMSWSPC 635  
Db 491 KALMCHIRKCEKTPMPAAEGTICGHEGA-GGQCVKYGDBGPKPTHGMSDMSWSPC 549  
Qy 636 SRTCGGVSHSR-LCTNPKPSHGKFCGSTRTLKLCNSQKCPRSDVDFRAAQCAEHNS 694  
Db 550 SRTCGGVSHSRQNTSHRPSHGKFCGSTRTLKLCNSQKCPRSDVDFRAAQCAEHNS 609  
Qy 695 RRFGRHYKMKPYQVEDDCLCYCIAEGFDFPFSLSKRVKXGDTFPCSEDSRNVCTDGC 754  
Db 610 RRFGRHYKMKPYQVEDDCLCYCIAEGFDFPFSLSKRVKXGDTFPCSEDSRNVCTDGC 664  
Qy 755 ERVGCNVLGSDAVEDVCGVCGNNSACTIHNGLTKKHHTTQYVMWVTPSGARSIRIY 814  
Db 665 ERVGCNVLGSDAVEDVCGVCGNNSACTIHNGLYL-----EYTHMVTTPSGARSIRIY 718  
Qy 815 EMNVSTSYISVNAALRRYYLNGHMTWDMGRYKFGTTFDYRSYNEPNLITATGPTNET 874  
Db 719 EMNVSTSYISVNAALRRYYLNGHMTWDMGRYKFGTTFDYRSYNEPNLITATGPTNET 778  
Qy 875 LIVELLFOGRNPGVAMEYMPRLGTEKOPAPDSTYWAIVRSECVSVCGGGCLPYLLLE 934  
Db 779 LIVELLFOGRNPGVAMEYMPRLGTEKOPAPDSTYWAIVRSECVSVCGGGCLPYLLLE 838

Oy 935 AACOPSATAYTALAFLES 952  
 |||||  
 Db 839 AACOPLATYITALAFLES 856  
 |||||  
 RESULT 9  
 US-10-399-645-4  
 ; Sequence 4, Application US/10399645  
 ; Publication No. US20040029249A1  
 GENERAL INFORMATION:  
 ; APPLICANT: INCYTE CORPORATION; LEE, Ernestine A.  
 ; APPLICANT: HAPFALIA, April J. A.; YUE, Henry  
 ; APPLICANT: LAU, Preeti G.; YAO, Monique G.  
 ; APPLICANT: LU, Yan; CHAWLA, Narinder K.  
 ; APPLICANT: WARREN, Bridget A.; LU, Dzung Aina M.  
 ; APPLICANT: BAUGHN, Marian R.; DELESEANE, Angelo M.  
 ; APPLICANT: LEE, Sally; XU, Yuming  
 ; APPLICANT: GRIFFIN, Jennifer A.; KALLITCK, Deborah A.  
 ; APPLICANT: GANDHI, Ameena R.; ARVIZU, Chandra S.  
 ; APPLICANT: ISON, Craig H.; TANG, Y. Tom  
 ; APPLICANT: AZIMZAI, Yalda; ELLIOTT, Vicki S.  
 ; APPLICANT: SWARNANAR, Anita; RAMKUMAR, Jayalaxmi  
 ; APPLICANT: NGUYEN, Daniel B.; TRIBOULEY, Catherine M.  
 ; APPLICANT: LO, Terence P.; AU-YOUNG, Janice K.  
 ; APPLICANT: THANGAVELU, Kavitha; KEARNEY, Liam  
 TITLE OF INVENTION: PROTEASES  
 FILE REFERENCE: PT-0263 USN  
 CURRENT APPLICATION NUMBER: US/10/399,645  
 CURRENT FILING DATE: 2003-04-16  
 PRIOR APPLICATION NUMBER: PCT/US01/51034  
 PRIOR FILING DATE: 2001-10-18  
 PRIOR APPLICATION NUMBER: US 60/241,573  
 PRIOR FILING DATE: 2000-10-18  
 PRIOR APPLICATION NUMBER: US 60/243,643  
 PRIOR FILING DATE: 2000-10-25  
 PRIOR APPLICATION NUMBER: US 60/245,256  
 PRIOR FILING DATE: 2000-11-02  
 PRIOR APPLICATION NUMBER: US 60/248,395  
 PRIOR FILING DATE: 2000-11-13  
 PRIOR APPLICATION NUMBER: US 60/249,826  
 PRIOR FILING DATE: 2000-11-16  
 PRIOR APPLICATION NUMBER: US 60/252,303  
 PRIOR FILING DATE: 2000-11-20  
 PRIOR APPLICATION NUMBER: US 60/250,981  
 PRIOR FILING DATE: 2000-12-01  
 NUMBER OF SEQ ID NOS: 30  
 SOFTWARE: PERL Program  
 ; SEQ ID NO 4  
 ; LENGTH: 1236  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc.feature  
 ; OTHER INFORMATION: Inctye ID No. US20040029249A1 3533147CD1  
 ; US-10-399-645-4  
 Query Match 52.8%; Score 3286; DB 15; Length 1236;  
 Best Local Similarity 93.1%; Pred. No. 1,3e-265;  
 Matches 591; Conservative 2; Mismatches 0; Indels 42; Gaps  
 Oy 334 HMPQPKEDLILPEYKSCLRHKRSILSRSHNEELANETVLVVDKMMQNHGHENITTY 393  
 :|||:|||||  
 Db 268 YMPQPKEDLILPEYKSCLRHKRSILSRSHNEELANETVLVVDKMMQNHGHENITTY 327  
 :|||:|||||  
 Oy 394 VLTILNVSALPKD-----GLMG 411  
 :|||:|||||  
 Db 328 VLTILNVSALPKDGTGGTTCGNNINIAVGLILDEDEPGVLVISHADHTLSSFCOMQSGLMG 387  
 :|||:|||||  
 Oy 412 KDGRRHDAIILTGDDISGWNKPCDTLGPAPISGMSKYSCTNEDTGGLATTAHE 471  
 :|||:|||||  
 Db 388 KDGRRHDAIILTGDDISGWNKPCDTLGPAPISGMSKYSCTNEDTGGLATTAHE 447  
 :|||:|||||

QY	412	SGHNFGMTHDESGNMCKKSEBNINSPITLAGNVPVSPSCROYLHKRLSTPAALCLADQ	531
Db	448	SGHNFGMTHDESGNMCKKSEBNINSPITLAGNVPVSPSCROYLHKRLSTPAALCLADQ	507
QY	532	PKPVKEYCPKLTDPGLDYDANTQCKWQGFGEKAKLCMLDFKDI CKALCFHRIGRKCTKF	591
Db	508	PKPVKEYCPKLTDPGLDYDANTQCKWQGFGEKAKLCMLDFKDI CKALCFHRIGRKCTKF	567
QY	592	MPAABGTT CGHDWMCRCGGQCVYKYGDEGPKPTHGHMSDMSSWSPCGRTCGGGVSHRSRLCT	651
Db	568	MPAABGTT CGHDWMCRCGGQCVYKYGDEGPKPTHGHMSDMSSWSPCGRTCGGGVSHRSRLCT	627
QY	652	NPKASHGKCFEESGTRTLKLCNSQCKCPDSDVPFAAOCAEHNSRRFRGRHKMKRYTOVE	711
Db	628	NPKASHGKCFEESGTRTLKLCNSQCKCPDSDVPFAAOCAEHNSRRFRGRHKMKRYTOVE	687
QY	712	DQDLCKLYCIAEGDFPFESLSNKKYVDGCPSCSEDSRMVCI DGI CERVGCDNYLGSDAVEDV	771
Db	688	DQDLCKLYCIAEGDFPFESLSNKKYVDGCPSCSEDSRMVCI DGI CERVGCDNYLGSDAVEDV	747
QY	772	CGVCGNNSACTTIRGLYTKHHNTNQYHMYTTPSGARSIIRIYEMNVSTSYISVENALRR	831
Db	748	CGVCGNNSACTTIRGLYTKHHNTNQYHMYTTPSGARSIIRIYEMNVSTSYISVENALRR	807
QY	832	YYLNGHMTVDPGRHYKKSCTTFEDYRSYNEPENI IANGPTNETLIVELLFGGRNVAME	891
Db	808	YYLNGHMTVDPGRHYKKSCTTFEDYRSYNEPENI IANGPTNETLIVELLFGGRNVAME	867
QY	892	YSMPRLGTEKOPPAQPSYTWAIIVSECSVSCGGGR	926
Db	868	YSMPRLGTEKOPPAQPSYTWAIIVSECSVSCGGGR	902
RESULT 10			
US-10-240-545A-2			
; Sequence 2, Application US/10240545A			
; Publication No. US20030185828A1			
; GENERAL INFORMATION:			
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.			
; TITLE OF INVENTION: No. US20030185828A1el1 aggrecanase			
; FILE REFERENCE: 08959.0002			
; CURRENT APPLICATION NUMBER: US/10/240.545A			
; CURRENT FILING DATE: 2002-10-02			
; PRIOR APPLICATION NUMBER: PCT/JP01/11033			
; PRIOR FILING DATE: 2001-12-17			
; PRIOR APPLICATION NUMBER: JP 2000-384300			
; PRIOR FILING DATE: 2000-12-18			
; NUMBER OF SEQ ID NOS: 26			
; SEQ ID NO 2			
; LENGTH: 1221			
; TYPE: PR			
; ORGANISM: Homo sapiens			
US-10-240-545A-2			
Query Match 46.5%; Score 2435.5; DB 14; Length 1221;			
Best Local Similarity 51.3%; Pred. No. 2-76-197;			
Matches 466; Conservative 118; Mismatches 155; Indels 129; Gaps 177;			
QY	85	ASSTGGAAGLDGKGRDMEAGNHRSOQTNTGTENTLHVLTOYDLVSAYEVDRHGRDYVS	144
Db	47	ASDSSGASGIN-----DDYVFVTPVEVDSAGSYIS	77
QY	145	HEIMHHQRRRAVAVSEVESLHLRLKGRPHDFHMDLTSSSLVAPGFIYQTLGKTGTSV	204
Db	78	HDILHNRKRRS-AQNARRSLHYFSAFGQGLHLELK-PSALISHTFIVQVLGXDGASET	135
QY	205	QTLPPEDFCFYQSLRSHRNSPSHGKFCBEGSTRTLKLCNSQ---KCPRDSVPFRAQC	260
Db	136	QK-QEVQCCFYQGITRND-SSSSVAVSTCAGLSGLIRTRKNEFLISPLPQ-----LLA	186
QY	261	AENHSRFRGRHYKMKRYTOVEADLCKLYCIAEGDFPFESLSNKKYVDG-----TPCSED	315



```

Db 187 QEHNYSPPAG-HHPVLYKRTAEKIQRKGYPG-----SGRNPYGSPSHIPIHASQS 238
Qy 316 R-----NVCIDGICELSVSTSAHMPOPPKEDLFLPDEYKSLRHRSLRS 363
Db 239 RETEYHRRLOKQHC-----GRKKYAPKPTEDTYLRFDEYSSGRPRBSAGS 289
Qy 364 HNEBELVETLVVVDKQMNQHNENITTYVLTILNMVSALFKDG-----408
Db 290 QKG--LNVETLVVADKKMVEKKGKGVNTTYILVTMMVNSGLFKDGTIGSDINVVVSLIL 347
Qy 409 -----LMKDGTRHDHAILLTGLDICSKNRPECPTLGF 441
Db 348 LEOPEGGLINHHADQSLNSFCQWOSALIGKNKRHDHAILLTGFDICSNKNEPCPTLGF 407
Qy 442 APISGMSKYRSCCTINEDTGLAFTIAHSGNFGMIDGEGNMCKSEGNIMSPYLAG 501
Db 408 APISGMSKYRSCCTINEDTGLAFTIAHSGNFGMIDGEGNMCKSEGNIMSPYLAG 467
Qy 502 RNVGFSWSPCSROYLHKFTLSTAOAICLADOPKVEKYKPEKLPGELDYDANTQCKWQFGR 561
Db 468 NNGVFSWSSCSROYLHKFTLSTAOAICLADOPKVEKYKPEKLPGELDYDANTQCKWQFGR 527
Qy 562 KATLCMLDFKXDCIKALMCHRIGRKCEKTPMPAEGTICSHDWCRGGQCVTKGDEGPRK 621
Db 528 KATLCMLDFKXDCIKALMCHRIGRKCEKTPMPAEGTICSHDWCRGGQCVTKGDEGPRK 587
Qy 622 THGWSWMSWSPCSRTCCGGVSHRSRLCTNPKPSHGKFCBEGSTRYLKLCNSQKCPRDS 681
Db 588 THGWSWMSWSPCSRTCCGGVSHRSRLCTNPKPSHGKFCBEGSTRYLKLCNSQKCPRDS 647
Qy 682 VDFRAAOCAEHNRRRPRGRHYKWKPYTOVEDODLCKLYCIAEGDFEFLSNKYKDGTPC 741
Db 648 LDFRAAOCAEYNKSPFRGWFYQKPKYTKVEEDRCLYCAENFEFFPMAKSGVKGOTPC 707
Qy 742 SEBSRVNCTIDGICERRGCONVLSDAVEDVCGVCGNNSACTIHRGLYTKHHTNOYTHM 801
Db 708 SPKNQNVCTIDGICELVCGCHELSKAVSDACGVCKGNSCKEYKGLYLNQHNANYYVP 767
Qy 802 VTPSGARSIRIYEMVNSTYISVRNALRYYLNGHMTVWPMGRYKPSGTFPDRSYNE 861
Db 768 VTPSGARSIRIYEMVNSTYISVRNALRYYLNGHMTVWPMGRYKPSGTFPDRSYNE 827
Qy 862 PENLIATGPTNETLIVELLFOGRNPGVAMEYSMPRL--GTEKOPRA--OPSYTMAIVRSE 917
Db 828 PENLIATGPTNETLIVELLFOGRNPGVAMEYSMPRL--GTEKOPRA--OPSYTMAIVRSE 884
Qy 918 CSVSCGGG 925
Db 885 CSVSCGGG 892

```

```

RESULT 11
US-10-363-937-17
; Sequence 17, Application US/10363937
; Publication No. US20040053269A1
; GENERAL INFORMATION:
; APPLICANT: Todd, Stephen; Delegeane, Angelo M.;
; APPLICANT: Gandhi, Ameena R.; Nguyen, Daniel B.;
; APPLICANT: Hafalia, April J.A.; Kearney, Liam;
; APPLICANT: Lu, Yan; Lee, Ernestine A.;
; APPLICANT: Chawla, Narinder K.; Das, Debopriya;
; APPLICANT: Arvizu, Chandra S.; Yao, Monique G.;
; APPLICANT: Kallick, Deborah A.; Elliott, Vicki S.;
; APPLICANT: Ding, Li; Yue, Henry;
; APPLICANT: Reddy, Roopa; Burford, Neil;
; APPLICANT: Baughn, Mariah R.; Lai, Preeci G.;
; APPLICANT: Boroweky, Mark L.; Lu, Dying Alina M.;
; APPLICANT: Ramkumar, Jayalaxmi; Yang, Junming;
; APPLICANT: Tribouley, Catherine M.; Khan, Farrah A.;
; APPLICANT: Gururajan, Rajagopal; Tang, Y. Tom;
; APPLICANT: Au-Young, Janice; Warren, Bridget A.;
; APPLICANT: Hernandez, Roberto; Duggan, Brendan M.
; TITLE OF INVENTION: PROTEASES

```

```

; FILE REFERENCE: PI-0212 USN
; CURRENT APPLICATION NUMBER: US/10/363,937
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: PCT/US01/28161
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: US 60/231,039
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232,812
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/234,850
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/236,500
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/238,773
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 60/239,658
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 1082
; TYPE: PRP
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20040053269A1 7478405CD1
US-10-363-937-17
Query Match 46.5%; Score 2434.5; DB 15; Length 1082;
Best Local Similarity 51.3%; Pred. No. 2.7e-197;
Matches 466; Conservative 118; Mismatches 195; Indels 129; Gaps 17;
85 ASSSTGAAGLGGKARDMDGAEHRSQQTNTGTENQTLVLTQYDLVSAEYDHGDIYS 144
47 ASDSSGASGLN-----DDYFVTFVPEVDSAGSYIS 77
145 HEIMHQRERRAAVAVSEVSLRLKGRPHDFMDLRTSSLVADGFVOTLGTGTYSV 204
78 HILHNGRKRS-AQNASLSHYRFAFGQELHLEK-PSAIISSHFIYQVLGKGASRT 135
205 QTLPEPDFYQGSLSRHSNPSHGKFCBEGSTRYLKLCNSQ---KCRSDVDFRAAO 260
136 QK-PEVOQCFYQGFTRND-SSSSVAVSTGAGLSGLIRRKMFLLISPLDQ-----LIA 186
261 AEHNSRRPRGRHYKWKPYTOVEDADLCKLYCIAEGDFEFLSNKYKDG-----TPCSEDS 315
187 QEHNYSPPAG-HHPVLYKRTAEKIQRKGYPG-----SGRNPYGSPSHIPIHASQS 238
Qy 316 R-----NVCIDGICELSVSTSAHMPOPPKEDLFLPDEYKSLRHRSLRS 363
Db 239 RETEYHRRLOKQHC-----GRKKYAPKPTEDTYLRFDEYSSGRPRBSAGS 289
Qy 364 HNEBELVETLVVVDKQMNQHNENITTYVLTILNMVSALFKDG-----408
Db 290 QKG--LNVETLVVADKKMVEKKGKGVNTTYILVTMMVNSGLFKDGTIGSDINVVVSLIL 347
Qy 409 -----LMKDGTRHDHAILLTGLDICSKNRPECPTLGF 441
Db 348 LEOPEGGLINHHADQSLNSFCQWOSALIGKNKRHDHAILLTGFDICSNKNEPCPTLGF 407
Qy 442 APISGMSKYRSCCTINEDTGLAFTIAHSGNFGMIDGEGNMCKSEGNIMSPYLAG 501
Db 408 APISGMSKYRSCCTINEDTGLAFTIAHSGNFGMIDGEGNMCKSEGNIMSPYLAG 467
Qy 502 RNVGFSWSPCSROYLHKFTLSTAOAICLADOPKVEKYKPEKLPGELDYDANTQCKWQFGR 561
Db 468 NNGVFSWSSCSROYLHKFTLSTAOAICLADOPKVEKYKPEKLPGELDYDANTQCKWQFGR 527
Qy 562 KATLCMLDFKXDCIKALMCHRIGRKCEKTPMPAEGTICSHDWCRGGQCVTKGDEGPRK 621
Db 528 KATLCMLDFKXDCIKALMCHRIGRKCEKTPMPAEGTICSHDWCRGGQCVTKGDEGPRK 587
Qy 622 THGWSWMSWSPCSRTCCGGVSHRSRLCTNPKPSHGKFCBEGSTRYLKLCNSQKCPRDS 681

```

Db 588 IHQWMSWMSWSCSRTCGGGVAFQEHHCNPKPQVGGIFCPGSSSHIYQICNINPCNENS 647  
Qy 682 VDFRAAQCAEHNSRRFRGRHYKMKPYQVEDODLCKLYCIAEGFDFPFSLSNKKVDTGC 741  
Db 648 LDFRAQCAEHNSKPRFGWYQMKPYTKYBEDRCKLYCAENFFPFSMSGKVXGDTGC 707  
Qy 742 SEDSRNVCIDGICEVYCDNLGSDAEDVCGVCGNNSACTIHRGLYTKHHTNOYTHM 801  
Db 708 SPKNQVNCIDGVCGLVGCHELGSKAVSDACGVCKDGNSTCKFYKGLYLNOHKAHEYFV 767  
Qy 802 VTFPSGARSIRIYEMNVSTYSIVRNALRRYLNHMTVDMPGRYKFSGTPDYRSYNE 861  
Db 768 VIIPGARSIEIQELQVSSSYLAVRSLQKTYLTGWSIDMPGEFPFAGTTEYQKSFNR 827  
Qy 862 PENLIATGPTNETLIVELLFQGRNPGVAMEYSMPRL--GTEKOPPA--OPSYTMAIVRSE 917  
Db 828 PERLYAAPFTNETLIVELLMOGKNPGIAMKVALPKVMNGT---PATRKRPAYTWSIVQSE 884  
Qy 918 CSVSCGGG 925  
Db 885 CSVSCGGG 892

RESULT 12  
US-10-354-983-2  
/ Sequence 2, Application US/10354983  
/ Publication No. US20040044194A1  
/ GENERAL INFORMATION:  
/ APPLICANT: AGOSTINO, MICHAEL J.  
/ APPLICANT: CORCORAN, CHRISTOPHER  
/ TITLE OF INVENTION: AGGRECANASE MOLECULES  
/ FILE REFERENCE: 08702.0111-00000  
/ CURRENT APPLICATION NUMBER: US/10/354,983  
/ PRIOR FILING DATE: 2003-01-31  
/ PRIOR APPLICATION NUMBER: 60/353,680  
/ PRIOR FILING DATE: 2002-01-31  
/ NUMBER OF SEQ ID NOS: 32  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 2  
/ LENGTH: 1221  
/ TYPE: PRF  
/ ORGANISM: Homo sapiens  
US-10-354-983-2

Query Match 46.5%; Score 2434.5; DB 15; Length 1221;  
Best Local Similarity 51.3%; Pred. No. 3.3e-197;  
Matches 466; Conservative 118; Mismatches 195; Indels 129; Gaps 17;  
Qy 85 ASSSTGAAGLDGKGRDMDGAGNHRGQNTNGTENGTLHVLTOYDVSAYEVDHRGDYVS 144  
Db 47 ASDSSSGAGGLN-----DDYVFTVEVDSDAGSYIS 77  
Qy 145 HEIMHHQRRRAVAVEVESLHLRLKGRPHDPMDLRTSSSLVAPGFITQLTGKTGSV 204  
Db 78 HDLHNGRKKRS-AQVARRSLHFRFAFGQELHLEK-PSALISSFIYQVLGKDGASST 135  
Qy 205 QTLPRDFCFYQSLRSHNSPSHGKFCFEGSTRLLKLCNSQ---KCPRDSVDFPRAOC 260  
Db 136 QK-PEVQCFYQGFIRND-SSSSVAVSTCAGLSGLIRTKRNEPLISPLQ-----LLA 186  
Qy 261 AEHNSRRFRGRHYKMKPYQVEDLCKLYCIAEGFDFPFSLSNKKVDTGC---TPCSEHS 315  
Db 187 QEHNSSPAG-HHPHLYKRTAEKIQRYRGYPG-----SGRNPYGSPSHIPRASGS 238  
Qy 316 R-----NVCIDGICELSVVSTSAHMPQRPEDLFTLPDEYKSCLRHKSILAS 363  
Db 239 RETEYHRRLLQKQHC-----GRKKYAPKPTTELTYYLRFDEYSGSGRRPSAGKS 289  
Qy 364 HNEBELNVELTVVVDKMQMNGHENITTYVLTILNVAALFKDG-----408  
Db 290 QKG--LNVETLVVADKKQVFKKGKGVVTTYLTLLVMMVSGLFDGTLGSDINVVVSLTL 347

Qy 409 -----LMKDGTRHDHAILLTGLDICSWKNEPCDITLGF 441  
Db 348 LEQEPGGLINNHADQSLNSFCQMSALIGKXKHHDAHLLTGFDCSWKNEPCDITLGF 407  
Qy 442 APIQMGSKYRSCSTINEDTGLAFTIAHSGHNGMIHDGSGNCKSEGINMSPTLGG 501  
Db 408 APIQMGSKYRSCSTINEDTGLAFTIAHSGHNGMIHDGSGNCFRQABGIMSPITLGG 467  
Qy 502 RNVGFSWSPCSRQYLAKFLSTAOALCLADQRPVREYKYPERLPEGLYDANTQCKMFGCE 561  
Db 468 NNGVFSWSPCSRQYLAKFLSTAOACLVDEPQAGQYKXPDLPQIYDADTQCKMFGCA 527  
Qy 562 KAKLCMLDPKDIICALMCHRIGRKCEYKFMNPAAGCTICGHDMCRGQCYKRYGBGPKP 621  
Db 528 KAKLCSLGFVKDICKSLWCHRGHRCETKFMNPAAGCTVCGSLMWCROQCYKRYGBGPKP 587  
Qy 622 TGHMSDMSWSPCSRQYGGVSHRSRLCTNPKPSHGKFCFEGSTRLLKLCNSOKPRDS 681  
Db 588 IHQWMSWMSWSCSRTCGGGVAFQEHHCNPKPQVGGIFCPGSSSHIYQICNINPCNENS 647  
Qy 682 VDFRAAQCAEHNSRRFRGRHYKMKPYQVEDODLCKLYCIAEGFDFPFSLSNKKVDTGC 741  
Db 648 LDFRAQCAEHNSKPRFGWYQMKPYTKYBEDRCKLYCAENFFPFSMSGKVXGDTGC 707  
Qy 742 SEDSRNVCIDGICEVYCDNLGSDAEDVCGVCGNNSACTIHRGLYTKHHTNOYTHM 801  
Db 708 SPKNQVNCIDGVCGLVGCHELGSKAVSDACGVCKDGNSTCKFYKGLYLNOHKAHEYFV 767  
Qy 802 VTFPSGARSIRIYEMNVSTYSIVRNALRRYLNHMTVDMPGRYKFSGTPDYRSYNE 861  
Db 768 VIIPGARSIEIQELQVSSSYLAVRSLQKTYLTGWSIDMPGEFPFAGTTEYQKSFNR 827  
Qy 862 PENLIATGPTNETLIVELLFQGRNPGVAMEYSMPRL--GTEKOPPA--OPSYTMAIVRSE 917  
Db 828 PERLYAAPFTNETLIVELLMOGKNPGIAMKVALPKVMNGT---PATRKRPAYTWSIVQSE 884  
Qy 918 CSVSCGGG 925  
Db 885 CSVSCGGG 892

RESULT 13  
US-10-120-801-48  
/ Sequence 48, Application US/10120801  
/ Publication No. US20030203843A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Pena, Carol  
/ APPLICANT: Guo, Xiaojia  
/ APPLICANT: Shinkets, Richard  
/ APPLICANT: Padigaru, Muralidhara  
/ APPLICANT: Kekuda, Ramesh  
/ APPLICANT: Spytek, Kimberly  
/ APPLICANT: Mehraban, Fuad  
/ APPLICANT: Topper, James N.  
/ APPLICANT: Maeserman, Scott  
/ APPLICANT: Edinger, Shlomit  
/ APPLICANT: Smithson, Glenda  
/ APPLICANT: Gunther, Erik  
/ APPLICANT: Komuves, Laszlo  
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
/ FILE REFERENCE: 21402-340  
/ CURRENT APPLICATION NUMBER: US/10/120,801  
/ PRIOR FILING DATE: 2002-04-11  
/ PRIOR APPLICATION NUMBER: 60/285748  
/ PRIOR FILING DATE: 2001-04-23  
/ PRIOR APPLICATION NUMBER: 60/286068  
/ PRIOR FILING DATE: 2001-04-24  
/ PRIOR APPLICATION NUMBER: 60/286292  
/ PRIOR FILING DATE: 2001-04-25  
/ PRIOR APPLICATION NUMBER: 60/288334  
/ PRIOR FILING DATE: 2001-05-03  
/ PRIOR APPLICATION NUMBER: 60/291241

/ PRIOR FILING DATE: 2001-05-16  
/ PRIOR APPLICATION NUMBER: 60/322284  
/ PRIOR FILING DATE: 2001-09-14  
/ PRIOR APPLICATION NUMBER: 60/285609  
/ PRIOR FILING DATE: 2001-04-20  
/ NUMBER OF SEQ ID NOS: 155  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 48  
/ LENGTH: 1365  
/ TYPE: PRF  
/ ORGANISM: human  
US-10-120-801-48

Query Match 46.4%; Score 2430; DB 15; Length 1365;  
Best Local Similarity 61.5%; Pred. No. 9.3e-197;  
Matches 479; Conservative 10; Mismatches 30; Indels 260; Gaps 10;

QY 335 MPQPPKEDLFLPDEYKSCLRHRSLSLRHNEBELVETLVVDDKMMQNHENITTYV 394  
DB 1 MPQPPKEDLFLPDEYKSCLRHRSLSLRHNEBELVETLVVDDKMMQNHENITTYV 60  
QY 395 LTLINVSALFKD-----GLMGK 412  
DB 61 LTLINVSALFKDGTGGNINIAIVGLILLEDROPGLVISHADHTLSSFCQMOGSLMGK 120  
QY 413 DGTGRDHAILLTGDLICSWKNEPCDTLGFAPISGMSKYSCTINEDTGLAFTIAHES 472  
DB 121 DGTGRDHAILLTGDLICSWKNEPCDTLGFAPISGMSKYSCTINEDTGLAFTIAHES 180  
QY 473 GH-----NFGMIHDG-----EGNM-----CKK 489  
DB 181 GHKGDYVEYSANYEWSRGMDSAREQATVPNRCCQLSLSPMEGELCFSRCLHEACVR 240  
QY 490 SEGNINISPTLA-----GRNGVFS-----WSPCSROYLHFLSTAQICL 528  
DB 241 ALGSSVLPVVAIIMPCKCGDSKTRGQALSCGGEKDRGNQFMSGRMSKVFGGTAQICL 300  
QY 529 ADQPKVKEYEYPEKLPGLDYANTOCQKQFGEKAKLCMLDPFK-----572  
DB 301 ADQPKVKEYEYBKLPGELDYANTOCQKQFGEKAKLCMLDPFKASMHNAQPREAGLYAR 360  
QY 573 -----DICKALWCHRIGRKCEKTFMPAAEGTI 599  
DB 361 SVQBASVSRGAQSLSLVSRDLSYCHPDIBPDICKALWCHRIGRKCEKTFMPAAEGTI 420  
QY 600 CGHDMCRGGQCYKYGDEGPKPTHGHSMSWSPGRTGGGVSHRSRLCTPKPSHG 659  
DB 421 CGHDMCRGGQCYKYGDEGPKPTHGHSMSWSPGRTGGGVSHRSRLCTPKPSHG 480  
QY 660 KFCGSTRTLKLCNSQKCPRDSYDFRAQCAEHNSRRFRGRHYKMKPYTOVEDODLCKLY 719  
DB 481 KFCGSTRTLKLCNSQKCPRDSYDFRAQCAEHNSRRFRGRHYKMKPYTOVE-----532  
QY 720 CIAEGFDPFPSLSNKVXDGTTPCSBDSHNVCI DGI CERVGCDNVLAGSDA VEDVCGVCNGNN 779  
DB 533 -----532  
QY 780 SACTIRGLYTKKHHNQYHMTIPSGARSIRIYENNVSTYSIVNALRYYLNGHW 839  
DB 533 -----EYHMYTIPSGARSIRIYENNVSTYSIVNALRYYLNGHW 575  
QY 840 VDMFGRYKFGSTFDYRSYNEPENLJATPTNETLIVELLFOGRNPGVAMEYMPPLGT 899  
DB 576 VDMFGRYKFGSTFDYRSYNEPENLJATPTNETLIVELLFOGRNPGVAMEYMPPLGT 635  
QY 900 EKQPPAPQSYTMAIVRSECVSGCG-----RCL-----FVLLLEAACQ 938  
DB 636 EKQPPAPQSYTMAIVRSECVSGCGGLNVCKFGALWKMGDYCLVPGDLHFLPLTSGCCQ 694

RESULT 14  
US-10-354-983-4  
Sequence 4, Application US/10354983

/ Publication No. US20040044194A1  
/ GENERAL INFORMATION:  
/ APPLICANT: AGOSTINO, MICHAEL J.  
/ APPLICANT: CORCORAN, CHRISTOPHER  
/ TITLE OF INVENTION: AGGREGANASE MOLECULES  
/ FILE REFERENCE: 08702.0111-00000  
/ CURRENT APPLICATION NUMBER: US/10/354,983  
/ PRIOR FILING DATE: 2003-01-31  
/ PRIOR APPLICATION NUMBER: 60/353,680  
/ PRIOR FILING DATE: 2002-01-31  
/ NUMBER OF SEQ ID NOS: 32  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 4  
/ LENGTH: 1071  
/ TYPE: PRF  
/ ORGANISM: Homo sapiens  
US-10-354-983-4

Query Match 46.1%; Score 2411.5; DB 15; Length 1071;  
Best Local Similarity 51.3%; Pred. No. 2.4e-195;  
Matches 466; Conservative 117; Mismatches 194; Indels 131; Gaps 19;

QY 85 ASSTTGAAAGLDGKGRDMDAGNHSQQTNTGTENQTLAVLYOYDLYSAVEVDHREDYVS 144  
DB 24 ASDSSGASAGLN-----DDYVVTPEVEDSAGSYIS 54  
QY 145 HEIMHQRBRRAVAVESEVSLHLRLKGRPHDFMDLRTSSLYAPGFIVQTLGKTGTSV 204  
DB 55 HDLHNGRKRKRS-AONARSSLHTRFSAFGOEHLLEK-PSAIISSFIYQVLKQDASER 112  
QY 205 QTLPEPDFCYOGLSLRHSNPSHGKFCGSTRTLKLCNSQ-----KCPRDSYDFRAAOC 260  
DB 113 QK-PEYQCFYQGFIND-SSSVAVSTCAGLSGLIRTKNEFLISPLPQ-----LLA 163  
QY 261 AEHSRRFRGRHYKMKPYTOVEDADLCKLYCIAEGFPFSSLSNKVXD-----TPCSBDS 315  
DB 164 OEHNSSPAG-HPHVLYKRTAEKIQRYRYPG-----SGRNPGYSPSHIIPIASOS 215  
QY 316 R-----NVCIDICELSVSTSAHMPQPPKEDLFLPDEYKSCLRHRSLSLS 363  
DB 216 RETEYHHRLOKQHC-----GRKKYAPKPTETTYLRFDEYSGSRPRRSAGS 266  
QY 364 HRNEBELVETLVVDDKMMQNHENITTYVTLINVSALFKD-----408  
DB 267 QKG-LNVEITLVADKKVVEKKGKGVTTYYLIVVMVSGLFQDGTGSDINVVVSLIL 324  
QY 409 -----LMKQDTRDHAILLTGDLICSWKNEPCDTLGF 441  
DB 325 LEOEPGGLLINHRADQSLNSFCQMOGSLIGKNGKRDHAILLTGDLICSWKNEPCDTLGF 384  
QY 442 APISGMSKYRSCCTINEDTGLAFTIAHESGNHFGMHDGSGMCKSEGNIMSPTLG 501  
DB 385 APISGMSKYRSCCTINEDTGLAFTIAHESGNHFGMHDGSGMCKSEGNIMSPTLG 444  
QY 502 RGVNFSWSPCSROYLHKLFLSTAQALICLADQPKVKEYEYKPEKLPGLDYANTOCQKQFGE 561  
DB 445 NNGVFSWSSCSRQYLKFLSTPQAGCLVDEPQAGQYKPRDLPGIYADDTCKMQFQA 504  
QY 562 KATLCMLDPKROI CKALWCHRIGRKCEKTFMPAAEGTITGHDWMCGGQCYKYGDEGPR 621  
DB 505 KATLCMLDPKROI CKALWCHRIGRKCEKTFMPAAEGTITGHDWMCGGQCYKYGDEGPR 563  
QY 622 TGHGMSWSPCSRTGGGVSHRSRLCTNPPPSHGKFCGSTRTLKLCNSQKCPRS 681  
DB 564 IHGQMSWMSKSECSRTGGGVSHRSRLCTNPPPSHGKFCGSTRTLKLCNSQKCPRS 623  
QY 682 VDFRAQCAEHNSRRFRGRHYKMKPYTOVEDODLCKLYCIAEGFDFFSLSNKVXDGTGC 741  
DB 624 LDFRAQCAEHNSRRFRGRHYKMKPYTOVEDODLCKLYCIAEGFDFFSLSNKVXDGTGC 683  
QY 742 SEDSRNVCTIDGICERYGCDNVLAGSDA VEDVCGVCNGNSACTIIRGLYTKKHHNQYH 801  
DB 684 SPNRNDVCTIDGICERYGCDNVLAGSDA VEDVCGVCNGNSACTIIRGLYTKKHHNQYH 742

```

OY      802 TTIPGASIRIYENNVSTSYISVYNALRRYYLNGHWYDMGGRYKFSSTEDYRSTYX 861
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      743 VIIIPGASISIEIQELQVSSSYIAVBSLSOKYLLTGSMSSIDWGEFFPAITTEYGRSENR 802
OY      862 PENLITATPTMETLIVELLFQGRNPGVAMEYEMPRU--GTEKQPA--OPSTMAIVSE 917
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      803 PERIYAPPTMETLIVFELLMQKNPGIAMKVALPKVMNCT---PATRKRPATWISIVQSE 859
OY      918 CYSVSCGGG 925
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      860 CYSVSCGGG 867

RESULT 15
US-10-120-801-46
; Sequence 46, Application US/10120801
; Publication No. US20030203843A1
; GENERAL INFORMATION:
; APPLICANT: Pena, Carol
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shinketsu, Richard
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Rameen
; APPLICANT: Spytek, Kimberly
; APPLICANT: Mehraban, Fuad
; APPLICANT: Topper, James N.
; APPLICANT: Malyankar, Uriel
; APPLICANT: Wasserman, Scott
; APPLICANT: Edinger, Shlomit
; APPLICANT: Smitsch, Glennda
; APPLICANT: Gutheer, Erik
; APPLICANT: Komuves, Laszlo
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-340
; CURRENT APPLICATION NUMBER: US/10/120, 801
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/285748
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 60/286068
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/286292
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/288334
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/291241
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/322284
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/285609
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 1081
; TYPE: PRT
; ORGANISM: human
US-10-120-801-46

Query Match      46.0%; Score 2408; DB 15; Length 1081;
Best Local Similarity 51.0%; Pred. No. 4,9e-195;
Matches 463; Conservative 118; Mismatches 197; Indels 130; Gaps 18

OY      85 ASSSTRGACGLDGKCRMDDEAGNRHSQOTNTGTENQTLHVLTOYLVSAIYEDHARGDYS 144
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      47 ASDSSSGASGN-----DDYVFVTPVEVDSAGSYIS 77

145 HEIMHQRARRAIVANVSEVESLHLRLKGPBPHMDLRTSSVAVAGFIYQTLGKTGTSV 204
DB      78 HDILHNKRKRS-AQNARSSLHYRISACQGLHLELK-PSALISHFIYQVLGKGASSET 135

OY      205 QTLPPEDCFYQGLSRHSRNSPSHGKFCESGSTRILKLCNSQ---KCPRDSVDFRAQC 260
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

Dd	136	QK-PEVQOCFQOGFIRND-SSSSVAVSTCAGLSGLIRRKNEFLISPLQO-----LLA	186
Qy	261	AEHNSRRFRGHYKWKRYTQVEADICLYCIAEGDFPFFSLSNKYKDQ-----TPCSEDS	315
Dd	187	QEHVYSSPAG--HHFVLTKRTAEKIQRYRGYQ-----SGRVYPGYSPSHI PHASOS	238
Qy	316	R-----NYCIDIGICELSVVSTSAHMPQPKEDFLLPREYXSLHHKBSLBS	363
Dd	239	KETEHYHRLQOKHFC-----GRKKYAPKEPTEBTYTRFBDYSSGRPRRAGKS	289
Qy	364	HNBEIYNETLVVDDKMMQNHGHENITTYVLTILNMVSALFPKQ-----	408
Dd	290	QKG--LWETLIVADKKVVEKHGKNVNTYILTWK--VSGLFKDGITGSDINVVVSLI	346
Qy	409	-----LMGODGTRHDHAILITGLDICSWKNEPCDTLGF	441
Dd	347	LEOEBGGLINHHDQSLNSFCQWOSALIKGKKGRKDHAILITGFPDICSWKNEPCDTLGF	406
Qy	442	APISGMSKYRSCITNEDTGLAFTIAHESGHNCGMIDHSGNCKXSEGNIMSTLAG	501
Dd	407	APTSGMSKYRSCITNEDTGLAFTIAHESGHNCGMIDHSGNCPRAKEGNIMSTLIG	466
Qy	502	RNGVFSWSPCSRQYILHKFLSTAQAICLADOPKRVEXKYPELJPELYDANTQCKQFGE	561
Dd	467	NGVFSWSSCSRQYILKFLSTPQAGCLVDEPRQAGQYKPRDLPGQIYADQTCCKQFGA	526
Qy	562	KAKICMLDFFKODICALMCHRIGRKCEKTEKMPAEGITCGHDMCKRGQOCVYKGEDEKPR	621
Dd	527	KAKICSLGFVNDICSLIMCHRVGNHCEKTEKMPAAGTQCGLSMCKRGQOCVYKGEJGAPRP	586
Qy	622	THGHMSDMSWSPCSRTOGGGVSHSRSLCTPKRPHGGKFCGSTRITLYLCSQKCPRS	681
Dd	587	IHGOWSANSKWSBESRTOGGGVKROBRKCNPKPQYGGIFCGSSRIYOLCINPNENBS	646
Qy	682	VDFAAOCAEHNSRRFRGRHYKWKRYTQVEBODLCKLYCIAEGDFPFFSLSNKYKDGTBC	741
Dd	647	LDFAAOCAEVNSKPRGWMFYQWKRYTQVEEBDRCLYCKAKENFEFFPFSMGKVXDGTBC	706
Qy	742	SEDSRNYCIDICERVGCNDVNLGSDAVEDVCGVCGNNSACTIHGGLYTKHHNTQYHM	801
Dd	707	SPNRKNDVICIDVCELVGCDHELGKAVASDACGVCGGDNSTCKFYGLYLNQHKANEYFV	766
Qy	802	VTIPSGARSIRIYENNVSTYSIVRNALRRARYLINHMTVDMGRKFKSGTTPDYRSVYE	861
Dd	767	VLPAGARSITIQELQVSSSYLARVSLSQCKYLLITGMSIDWDEEPPFAGTIEYQHSNR	826
Qy	862	PENLIATGPTIETLIVELLFQGRNPGVAMWBSMPL--GTEKQPPA--QPSYTMALVRSE	917
Dd	827	PERLYAPGPTIETLYPEILMOGKNPGLMIKVALPKVMNGT---PATKRPATYTWISVQGE	883
Qy	918	CSVSCGGG 925	
Dd	884	CSVSCGGG 891	

Search completed: September 9, 2005, 23:48:58  
Job time : 1305 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OW protein - nucleic search, using frame\_plus\_p2n model

Run on: September 9, 2005, 22:16:24 ; Search time 375 Seconds  
(without alignments)  
4153.961 Million cell updates/sec

Title: US-09-981-151D-8  
Perfect score: 5236  
Sequence: 1 MKPRARGMGLAAMWLAQ.....LEAACQPSATAYATLAFLES 952

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Delop 6.0 , Delext 7.0

Searched: 1202784 segs, 818138359 residues  
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+ p2n.model -DEV=xlp  
-Q=/cgn2\_1/USFTO\_spool\_p/US09981151/runat\_07092005\_173417\_18697/app\_query.fasta\_1.1095  
-DB=Issued Patents NA -QPMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPEXT=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pcc -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09981151 @CGN 1.1.105 @runat\_07092005\_173417\_18697 -NCP1=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:\*  
1: /cgn2\_6/prodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/prodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/prodata/1/ina/PCITUS\_COMB.seq:\*  
6: /cgn2\_6/prodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	3981.5	76.0	3675	3	US-09-930-872-3
2	3981.5	76.0	3675	4	US-10-217-774-3
3	3981.5	76.0	4042	3	US-09-930-872-5
4	3981.5	76.0	4042	4	US-10-217-774-5
5	1678.5	32.1	1476	3	US-09-930-872-1
6	1678.5	32.1	1476	4	US-10-217-774-1
7	1390	26.5	2727	4	US-09-963-791-1
8	1319	25.2	2274	4	US-09-963-791-1
9	1294	24.5	3160	4	US-09-963-791-25
10	1247.5	23.8	3571	4	US-09-799-451-411
11	1245.5	23.8	5357	3	US-09-392-184-5
12	1243	23.7	3377	4	US-09-981-953A-3

13	1237	23.6	3766	4	US-09-981-953A-1	Sequence 1, Appl1
14	1218	23.3	2848	3	US-09-369-364A-4	Sequence 4, Appl1
15	1186	22.7	3218	3	US-09-369-364A-6	Sequence 6, Appl1
16	1102.5	21.1	3885	3	US-09-369-364A-16	Sequence 16, Appl1
17	1056	20.2	5804	3	US-09-369-364A-12	Sequence 12, Appl1
18	1010	19.3	4676	3	US-09-130-491-1	Sequence 1, Appl1
19	997.5	19.1	3889	4	US-09-568-559-1	Sequence 1, Appl1
20	997	19.0	4858	3	US-09-392-184-1	Sequence 1, Appl1
21	991	18.9	2625	3	US-09-369-364A-14	Sequence 14, Appl1
22	969	18.5	6659	4	US-09-321-987B-1	Sequence 1, Appl1
23	961.5	18.4	4580	3	US-09-491-522-8	Sequence 8, Appl1
24	958.5	18.3	3184	4	US-09-445-023A-13	Sequence 13, Appl1
25	949	18.1	3636	4	US-09-949-016-5530	Sequence 530, Ap
26	942.5	18.0	6592	4	US-09-491-522-1	Sequence 1, Appl1
27	934	17.8	2184	4	US-09-445-023A-2	Sequence 2, Appl1
28	929.5	17.8	2853	4	US-10-009-332-2	Sequence 2, Appl1
29	920.5	17.6	3706	3	US-09-484-970B-58	Sequence 58, Appl1
30	917	17.5	2450	3	US-09-491-522-2	Sequence 2, Appl1
31	912.5	17.4	2450	3	US-09-491-522-9	Sequence 9, Appl1
32	885.5	16.9	3002	3	US-09-369-364A-1	Sequence 1, Appl1
33	878	16.8	3250	3	US-09-122-126B-14	Sequence 14, Appl1
34	878	16.8	3250	4	US-09-634-286A-14	Sequence 14, Appl1
35	878	16.8	3250	4	US-10-247-685-14	Sequence 14, Appl1
36	856.5	16.4	4192	3	US-09-122-126B-1	Sequence 1, Appl1
37	856.5	16.4	4192	4	US-09-634-286A-1	Sequence 1, Appl1
38	856.5	16.4	4192	4	US-10-247-685-1	Sequence 1, Appl1
39	839.5	16.0	3638	3	US-09-369-364A-8	Sequence 8, Appl1
40	776.5	14.8	1770	4	US-09-963-791-11	Sequence 11, Appl1
41	755.5	14.4	3126	4	US-09-392-184-7	Sequence 7, Appl1
42	705.5	13.5	1317	4	US-09-963-791-21	Sequence 21, Appl1
43	607	11.6	2114	4	US-09-130-491-7	Sequence 7, Appl1
44	578.5	11.0	1524	4	US-09-963-791-9	Sequence 9, Appl1
45	550	10.5	3158	4	US-09-949-016-1988	Sequence 1988, Ap

ALIGNMENTS

RESULT 1  
US-09-930-872-3  
; Sequence 3, Application US/09930872  
; Patent No. 6448388  
; GENERAL INFORMATION:  
; APPLICANT: Fiddie, Carl Johan  
; APPLICANT: Hilbun, Erin  
; TITLE OF INVENTION: No. 6448388 Human Proteases and Polynucleotides Encoding the San  
; FILE REFERENCE: LEX-0219-USA  
; CURRENT APPLICATION NUMBER: US/09/930,872  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: US 60/225,852  
; PRIOR FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 3675  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-930-872-3  
  
Alignment Scores:  
Pred. No.: 0  
Score: 3981.50  
Percent Similarity: 78.26%  
Best Local Similarity: 76.55%  
Query Match: 76.04%  
DB: 3  
Gaps: 10  
  
US-09-981-151D-8 (1-952) x US-09-930-872-3 (1-3675)  
  
QY 1 MetLysProArAlaArgLyTPArGlyLeuAlaLeuTropwLeuLeuAlaGln 20  
Db 1 ATGAAAGCCCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60  
QY 21 VALAlaGluGlnValSerProGlyArgSerH1sgInArgLyAsnArgLySerGlyGln 40

Db 61 GTGGCCGAGCA----- 71  
Qy 41 LeuGluAlaSerProProAlaGluLeuSerArgGlyProArgArgLeuThrAlaMetSer 60  
Db 71 ----- 71  
Qy 61 ProLeuPheSerAlaGlyThrCysValArgHisGlyThrArgSerGlySerAlaTyrGly 80  
Db 72 -----GAGCACTGCGTGGCCATGGAGCCCGGACCGGACCGGCGCTGGGAG 116  
Qy 81 ProGluArgProAlaSerSerSerThrArgGlyAlaAlaGlyLeuAspArgGly-LysGlyArg 100  
Db 117 CCGAGACGTCGCGCGCTCTCCACCGCGAGACCGCGCGCTGAGATGGAAAAAGGCGC-- 174  
Qy 100 GAspMetAspGluAlaGlyAsnHisArgSerGlnGlnThrAsnThrGlyThrGlyAsnGly 120  
Db 174 ----- 174  
Qy 120 nThrLeuHisValLeuThrGlnTyrArgLeuValSerAlaTyrGlyValAspHisArgGly 140  
Db 175 -----GAATATGACCTGGTCTCTGGCTTACGAGGTTGACCAACAGGGG 215  
Qy 140 YAspTyrValSerHisGlyLeuLeuMetHisGlnArgArgArgAlaValAlaValSer 160  
Db 216 CGATTACGTGCCATGAAATCATGCAACATCAGCGCGAGAAAGCAAGTGGCGCTGTGC 275  
Qy 160 rGluValGluSerLeuHisValArgLeuLysGlyProArgHisAspPheHisMetAspLe 180  
Db 276 CGAGGTGAGTGTCTTCACTTCGGCTGAAGGCTCCAGGACGATTCACACGTGATGTC 335  
Qy 180 YArgThrSerSerSerLeuValAlaProGlyPheLeuValGlnThrLeuGlyLysThrGly 200  
Db 336 GAGGACTTCAGACAGCTGAGTGGCTCTGGCTTATTTGTGCAGACCTTGGGAAAGCACAG 395  
Qy 200 YThrLysSerValGlnThrLeuProProGluAspPheCysPheTyrGlnGlySerLeuArg 220  
Db 396 CACTTAAGTCTGTGCAACATTACCGCACAGACCTGTGTCTTATCAAAAGGCTTTGGG 455  
Qy 220 gSerHisArgAsnSerProSerHisGlyGlyLysPheCysGlnGlySerThrArgThrHis 240  
Db 456 ATCACAACAGAACTCC--TCAAGTGGCCCTTCAACCTGCAGAAAGCTTGACGCAATGAT 512  
Qy 240 YLysLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaAlaGlnCys 260  
Db 513 ACGA-----ACAGAAAGGCAAGATTAATCTCTTAAGGCACT 548  
Qy 260 sAlaGluHisAsnSerArgArgPheArgGlyArgHisTyrLysTyrLysProTyrThrGly 280  
Db 549 TCCTTCAACCTCTCA-----TGGAA----- 570  
Qy 280 nValGluAlaAspLeuCysLysLeuTyrCysAla-AlaGlnGlyPheAspPhePhePheS 300  
Db 571 -----CTCGGCAAGG----- 580  
Qy 300 eLeuSerLeuLysValLysAspGlyThrProCysSerGlyLysSerArgAsnValCysI 320  
Db 581 --CTGCCCAAGGAGCTCGGCATCCCAAGTACTGTACAGAGATCCACAGAGCCCATGC 638  
Qy 320 lAspGlyTyrLeuCysGlyLeuSerValValSerThrSer-----AlaHis----- 334  
Db 639 TCCT--GGGGCCAGTGAAGTCTGGTGAACCTCAAGACATGGAGCTGGACATCAACCCC 697  
Qy 334 ----- 334  
Db 698 TGCACAGCAGCAGCACTTGGCTGGAGCTGCACAAAAGCAGATTTCTTGGAAAGCAGCA 757  
Qy 335 -----MetProGlnProProLysGlyLysAspLeuPheLeuProAspGlyTyrLys 352  
Db 758 AGAAATACATGGCCCCAGCTCCCAAGAAAGACCTTTCATCTTGCAGATGAGTAAAGT 817  
Qy 352 eCysLeuArgHisLysArgSerLeuLeuArgSerHisArgArgGlnGlyLysAsnValG 372

Db 818 CTTCCTTAAGCCAGTAAGGCTCTCTTCTGAGGTCCCATTAAGAAATGAAATGAAACGTGG 877  
Qy 372 lThrLeuValValValAspLysLysMetMetGlnAsnHisGlyLysLysAsnLeuThrT 392  
Db 878 AGACCTTGGTGGTGGTCCGACAAAAGATGATGCABAAACCATGGCCATGAAATATCACCA 937  
Qy 392 hTyrValLeuThrLysLeuAsnMetValSerAlaLeuPheLysAsp----- 407  
Db 938 CTTAGGTGTACGATTAATCAACATGTATCTGTATTCTTAAGATGACAAATAGAGAG 997  
Qy 407 ----- 407  
Db 998 GAAACATCAACATTGCAATTGAGTCTGATTTCTTGAAGATGAAACCCAGACTGG 1057  
Qy 408 -----GlyLeu 410  
Db 1058 TGATTAAGTACACGACGACAGCACACACTTAAGAGCTTGGCAGTGGAGCTGGATTGA 1117  
Qy 410 eGlyLysAspGlyThrArgHisAspHisValAlaLysLeuLeuThrGlyLeuAspLysCys 430  
Db 1118 TGGGAAAGATGGGACTGCTCATGACCAAGCCATCTTACTGACTGCTGGATATATGTT 1177  
Qy 430 eTyrLysAsnGluProCysAspThrLeuGlyPheAlaProLysSerGlyMetCysSerL 450  
Db 1178 CTTGGAAGATGAGCCCTGTGACCTTGGATTTGGACCCATTAAGTGAATGTGTAGTA 1237  
Qy 450 YTyrArgSerCysThrLysAsnGluAspThrGlyLeuGlyLeuAlaPheThrLysAla 470  
Db 1238 AATATCGCAGCGTGCAGATTATGAAGATACAGGCTTGGACTGGCTTCACATTTGCC 1297  
Qy 470 lGluSerGlyHisAsnPheGlyMetLeuLysAspGlyGlnGlyLysMetCysLysLys 490  
Db 1298 ATGAGTCTGGACACAACTTTGGCATGATTCATGAAGGAAAGGAAACATGTGTAAAAAGT 1357  
Qy 490 eGlnGlyAsnHisMetSerProThrLeuAlaGlyArgAsnGlyValPheSerTyrSerP 510  
Db 1358 CCGAGGGAACATCATGTCCTCCCTACATTGGCAGACGCAATGAGTCTTCTCTGTGCAC 1417  
Qy 510 rCysSerArgGlnTyrLeuHisLysPheLeuSerThrAlaGlnAlaLysCysLeuAla 530  
Db 1418 CTTGAGCGCGCAGATCTTACCAAAATTTTAAGCACCGCTCAAGCTATCTGCTTGGTG 1477  
Qy 530 sPrlnProLysProValLysGlyTyrLysTyrProGluLysLeuProGlyGluLeuTyr 550  
Db 1478 ATCAGCCAAAGCTGTGAAGAAATACAAATATCCGAAAAATGGCAGAGAAATATATG 1537  
Qy 550 sPrlaAsnThrGlnCysLysTyrProGlnPheGlyGlnLysAlaLysLeuCysMetLeuAsp 570  
Db 1538 ATGCAAAACACAGTGCAGTGGCGATTCGAGAGAAAGCCAAAGCTTGATGCTGGACT 1597  
Qy 570 hElyLysAspLysCysLysValLeuTyrCysHisArgLysGlyArgLysCysGlnThrL 590  
Db 1598 TTAAAAAGACATCTGTAAGCCCTGTGGTCCATCGATTTGAAAGAAATGTGAGACTA 1657  
Qy 590 YAspMetProAlaAlaGlnGlyThrLysCysGlyHisAspMetTyrCysArgGlyGlyG 610  
Db 1658 AATTATATCCACAGCAGCAAGACCAATTTGTGGCATAAGCATGTGGTGCCGGAGAGAC 1717  
Qy 610 lNysValLysTyrGlyAspGlyLysProLysProThrHisGlyHisTyrSerAspTyrS 630  
Db 1718 AGTGTGAATATATGTATATGAAGCCCCCAAGCCCAAGCCCAAGCTGGTGGACTGGT 1777  
Qy 630 eTyrTyrSerProCysSerArgThrCysGlyGlyValSerHisArgSerArgLeu 650  
Db 1778 CTTCTTGTCCCATAGTCCAGAACCTCGGAGGGGAGTATCTCATATGAGATGCTCTCT 1837  
Qy 650 YThrAsnProLysProSerHisGlyGlyLysPheCysGlnGlySerThrArgThrLeu 670  
Db 1838 GCACCAACCCCAAGGCATCGATGAGGAGAAATTTCTGAGAGGGCTCCACTGCACCTTGA 1897  
Qy 670 YLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaAlaGlnCys 690  
Db 1898 AGCTTGCACAGTCAAGAAATGTCCCGGAGACATGTATGACTTCGCTGCTCAAGTGTG 1957

```
QY 690 lAgIuHlSaAnSeArArGArGPhEArGlyArGhIeTyLySTrLyPrTyThrGlnV 710
    |||||
Db 1958 CCGAGCACAAACAGCAGCCATTTCAGAGGGCGGCATCAAGTGGAAAGCCTTACACTCAAG 2017
QY 710 aIGlUaErglNaEpleuCyblyeLeuTyCyblllealagluGlyPheApePhePheS 730
    |||||
Db 2018 TTAGAAGATCAGGACCTTATGCAACTCTACTGTATCCGAGAAAGATTGATTTCTCTTTT 2077
QY 730 eRleuSeArSeNlyVaLySaErglYThrProCySeSerGluAaPeSeArGArGValCyel 750
    |||||
Db 2078 CTTTGTCATTAATTAAGTCAAGATGGAATCTCATGCTCCGAGAGAGCCGTAATGTTTGA 2137
QY 750 lEaPeRgLyIleCybglUaErgValGlyCySaPaSaNaValleuGlySeArPaAlaValGluA 770
    |||||
Db 2138 TTAGATGGAGATATGAGAGAGCTTGATGTGACATGCTCTTGATCTGAGTCTGTTGAAG 2197
QY 770 ePValCySeGlyValCySaErglyAaNaPeSeRAlaCySThrllleHlSaErglyLeuTyT 790
    |||||
Db 2198 ACCTCTGTGGGTGTGTAAACGGGAATTAACACCTGACAGATTCAACAGGGGTCTCTACA 2257
QY 790 hRlyeHlSHlSHlSThPaErglNlyTyThlSMeValThrlleProSeRgLyAlaArgS 810
    |||||
Db 2258 CCAAGCACCAACCAACCAAGATTAATCAAGTCAATTCCTCTGAGAGCCGGA 2317
QY 810 eRlleArGlyleTyGluMeArNaValSeRThSeTyTyllSeSeRValArGAsnaAlaEua 830
    |||||
Db 2318 GTATCGGCATCTAATAATGAAGTCTCTACCTCTCAATTTCTGTGCGGAAGCCCTCA 2377
QY 830 rGArGTyTyTyLeuAeNglyHlSTrThVaLapTrProGlyArGTyTyTyLePheSeRg 850
    |||||
Db 2378 GAAGGTACTTACCTGAATGGGCACCTGACCTGACCTGCCGCCGCTACAATTTTCCG 2437
QY 850 lYThlrThrPheArPyTyArGArGSeTyThPaErglUaPeNleuHlleaThGlyP 870
    |||||
Db 2438 GCACTACTTTCGACTACAGAGGCTCTTAATATAGCCCGAAGCTTAATGCTACGTGAC 2497
QY 870 rOThPaErglUaThrLeuHlleaIGlUleuPeNheGnglyArGAsnaProGlyValAlaT 890
    |||||
Db 2498 CAACCAACGAGACACTGATTGTGAGCTGCTGTTTACAGGAAAGAACCCGGGTGGCT 2557
QY 890 rPglUtySeRSeTProArGleuGlyThrGluYsglProPAlaGlnProSeTyT 910
    |||||
Db 2558 GGGAAATATCTCCATGCTCGCTTGCGGACCGAAGAGAGCCCCCTGCCACAGCCCACTACA 2617
QY 910 hTTrPaAlleValArGSeRglUaCySeRValSeCySglYglYArG 926
    |||||
Db 2618 CTGGGCATGTCGCTGAGTGTCTGCTGTCTGCGAGGGGAGACAG 2667
```

```
RESULT 2
US-10-217-774-3
; Sequence 3. Application US/10217774
; Patent No. 6734007
```

```
; GENERAL INFORMATION:
; APPLICANT: Fiddie, Carl Johan
; APPLICANT: Hilbun, Erln
; TITLE OF INVENTION: No. 6734007el Human Proteases and Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/10/217,774
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/930,872
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3675
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-774-3
```

## Alignment Scores:

Pred. No.:	0	Length:	3675
Score:	3981.50	Matches:	764
Percent Similarity:	78.26%	Conservative:	17
Best Local Similarity:	76.55%	Mismatches:	38
Query Match:	76.04%	Indels:	181
DB:	4	Gaps:	10

US-09-981-151D-8 (1-952) x US-10-217-774-3 (1-3675)

```
QY 1 MeLySPrOArGAlaRgLyThrArGlyLeuAlaAlaLeuTryMetLeuLeuAlaGln 20
    |||||
Db 1 ATGAAGCCCCCGCGCGGATGGCGGAGCTTGCGCGCTGTGATGCTGCGCGAG 60
QY 21 ValAlaGluGlnValSeRProGlyArGSeRhlSGlnArGlyAaNaRgLySeRgLyGln 40
    |||||
Db 61 GTGGCCGAGCA----- 71
QY 41 LeuGluAlaSeRProArGleuLeuSeArArGlyProArGArGleuThrAlaMetSeR 60
    |||||
Db 71 ----- 71
QY 61 ProLeuPheSeRAlaGlyThrCySaValArGhIeGlyThrArGSeRgLySeRAlaTrGln 80
    |||||
Db 72 -----GGCACTGTGCGCGCATGGGACCGGACCGGACCGCGCTGCGGAG 116
QY 81 ProGluArGProAlaSeSeSeSeRThrArGgLyAlaAlaGlyLeuApeRgLy- LySglYAr 100
    |||||
Db 117 CCGAGAGCTCCGCGCTCTCTCCACCCCGAGAGCGGCGGGCTGATGGAAAGGCG-- 174
QY 100 gAPMeTaErglUaAlaGlyAaNHlSaRgSeRglnThrAeNthrglyThrGluAeNg 120
    |||||
Db 174 ----- 174
QY 120 nThrleuHlSHlSHlSThPaErglUaPeNleuHlleaThrGlyValaLapRhlSaRgG 140
    |||||
Db 175 -----GAATATGACCTGGTCTCTGCTTGCAGAGTTCACAGCGGAG 215
QY 140 yAPeTyTyTyLeuHlSHlSHlSHlSHlSHlSHlSHlSHlSHlSHlSHlSHlSHlSHlSHl 160
    |||||
Db 216 CGATTACGTCTCCATGAATATGATGACATGACGCGCGGAGAAAGACAGTGGCGCTGTC 275
QY 160 rGluValGluSeRleuHlSHlSHlSHlSHlSHlSHlSHlSHlSHlSHlSHlSHlSHlSHlSHl 180
    |||||
Db 276 CGAGGTGAGTCTCTTCACTTCGAGTAAAGCTTCACAGCAAGCTTCACAGTGGATCT 335
QY 180 uArGThrSeRSeSeSeSeSeSeSeSeSeSeSeSeSeSeSeSeSeSeSeSeSeSeSeSeSe 200
    |||||
Db 336 GAGGACTTCACAGAGCTATGAGCTCTCTGCTTATTTGACAGACGTTGGAAAGACAG 395
QY 200 yThrlySeSeValGlnThrLeuProProGluAaPePheCySPhetyTyGlnGlySeRleuAr 220
    |||||
Db 396 CACTAAGTCTGTGACACTTTTACCGGCAAGAGACTTCTTTCTATCAAGGCTCTTTGGG 455
QY 220 gSeRhlSaRgAsSeRProSeRhlSHlSHlSHlSHlSHlSHlSHlSHlSHlSHlSHlSHlSHl 240
    |||||
Db 456 ATCAGACAGAAACTCC---TCAGTGGCCCTTCAACCTCCCAAGGCTTTCAGGACATGAT 512
QY 240 uLySeLeuCySaErglUaCySaErglUaPeRSeRValaPeRSeRValaAlaGlnCy 260
    |||||
Db 513 ACGA-----ACAGAAAGGACGATTTACTTCTTAAGGCACT 548
QY 260 bAlaGluHlSaAnSeArArGArGPhEArGlyArGhIeTyLySTrLyPlyPrTyThrGln 280
    |||||
Db 549 TCCTTCACACCTCTCA-----TGAAA----- 570
QY 280 nValGluAlaPeRleuCyblyeLeuTyCySllle- AlaGluGlyPheApePhePheS 300
    |||||
Db 571 -----CTCGGCAAG----- 580
QY 300 eRleuSeArSeNlyVaLySaErglYThrProCySeSerGluAaPeSeArGArGValCyel 320
    |||||
Db 581 --CTGCCAAGGAGCTGCGCATCCACAGCTACTGTATCAAGAGATCCACAGAGCCCATGTC 638
```





```
/ CURRENT APPLICATION NUMBER: US/09/930,872
/ CURRENT FILING DATE: 2001-08-14
/ PRIOR APPLICATION NUMBER: US 60/225,852
/ PRIOR FILING DATE: 2000-08-16
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: FaSTSeq for Windows Version 4.0
/ SEQ ID NO 5
/ LENGTH: 4042
/ TYPE: DNA
/ ORGANISM: homo sapiens
US-09-930-872-5

Alignment Scores:
Pred. No.: 0 Length: 4042
Score: 3981.50 Matches: 764
Percent Similarity: 78.26% Conservative: 17
Beet Local Similarity: 76.55% Mismatch: 38
Query Match: 76.04% Indels: 181
DB: Gaps: 10

US-09-981-151d-8 (1-952) x US-09-930-872-5 (1-4042)

QY 1 MetLysProArgAlaArgGlyTTrArgGlyLeuAlaAlaLeuTTrMetLeuLeuAlaGln 20
DB 99 ATGAAGCCCGCCGCGCGGATGGCGGCGCTTGCGCGCGCTGTGAGATGCTGGCGCAG 158
QY 21 ValAlaGluGlnValSerProGlyArgSerHisGlnArgGlyValnArgGlySerGlyGln 40
DB 159 GTGGCCGAGCA----- 169
QY 41 LeuGluAlaSerProArgLeuLeuSerArgGlyProArgArgLeuThrAlaMetSer 60
DB 169 ----- 169
QY 61 ProLeuPheSerAlaGlyThrCyValArgHisGlyYThrArgSerGlySerAlaTrrGly 80
DB 170 -----GGCACTGCGTGGCGCCATGGGACCCGACGCGGCAAGCGCTGGAG 214
QY 81 ProGluArgProAlaSerSerSerThrArgGlyAlaAlaGlyLeuArgGly-LysGlyArg 100
DB 215 CCGGAGCGTCCCGGCTCTCTCCACCCGCGAGCGGCGGCGCTGGAGTGAAGAGGCG-- 272
QY 100 GArMetAspGluAlaGlyValnHisArgSerGlnGlnThrAsnThrGlyYThrGluAsnG 120
DB 272 ----- 272
QY 120 nThrLeuHisValLeuThrGlnTyrThrAspLeuValSerAlaTyrGluValAspHisArgG 140
DB 273 -----GAAATATGACCTGGTCTGCTGCTTACGAGGTTGACCAAGGGG 313
QY 140 YAspTyrValSerHisGlnLeuMetHisGlnArgArgArgAlaValAlaValSe 160
DB 314 CGATTACGTCCTCCAGAAATCATGACCATCAGCGCGGAGGAAGAGCACTGGCCGTC 373
QY 160 rGluValGluSerLeuHisLeuArgLeuLysGlyProArgHisAspPheHisMetAspLe 180
DB 374 CGAGGTGAGTCTCTTACCTTGGCTGAGAAAGGCTCCAGGCAAGCATTCACAGTGATCT 433
QY 180 YArgThrSerSerSerLeuValAlaProGlyPheHisGlnThrLeuGlyYThrGln 200
DB 434 GAGAGCATTCACAGCAAGCTAGTGGCTCTGCTTATTTGTGCAGACGTTGGGAAGACAG 493
QY 200 YThrLysSerValGlnThrLeuProArgProGluAspPheCysPheTyrGlnGlySerLeu 220
DB 494 CACTTAAGTCTGTGACAGCTTACCGCCAGAGACTTCTGTTCTATTCAGAGCTCTTGG 533
QY 220 gSerHisArgAsnSerProSerHisGlyGlyYValPheCyGluGlySerThrArgThr 240
DB 554 ATCACAACAGAAACTCC--TCAGTGGCCCTTCAACTGCCAAGGCTGTGCAGGATGAT 610
QY 240 uLysLeuCyAsnSerGlnLysCyAspArgAspSerValAspPheArgAlaAlaGlnCy 260
DB 611 ACGA-----ACAGAAAGGCGAGATTACTTCTTAAGGCGCACT 646
```

```
QY 260 sAlaGlnHisAsnSerArgArgPheArgGlyArgHisTyrLysTrrLysProTyrThrGln 280
DB 647 TCCTTCACACCTCTCA-----TGGAAA----- 668
QY 280 nValGluAlaAspLeuCyValLeuTyrCySile-AlaGluGlyPheAspPhePhePhe 300
DB 669 -----CTCCGCAAG----- 678
QY 300 eTrLeuSerAsnLysValLysAspGlyThrProCySerGlnLysAspSerArgAsnValCys 320
DB 679 --CTGCCAAGGCAAGCTGCCCATCCCAAGTACTGTATCAAGATCCACAGAGCCCATGC 736
QY 320 LeAspGlyLLeCySylLeuSerValValSerThrSer-----AlaHis----- 334
DB 737 TCCT-GGGGCGAGTAGAGTCTGTGTATCCTCAAGACATGGGAGCTGGACATCAAGCC 795
QY 334 ----- 334
DB 796 TGCACAGACGACCTTCCGCTGGACTGCCAAGAAAGCATTTCTGTGAGAGAGCGCA 855
QY 335 -----MetProGlnProProLysGluAspLeuPheHisLeuProArgGlyLys 352
DB 856 AGAATATCATGCCCGCCAGCTCCCAAGAAAGACTTTCATCTTGCCAGATGAGTATAGT 915
QY 352 eCySerLeuArgHisLysArgSerLeuLeuArgSerHisArgAsnGluGluLeuAsnValG 372
DB 916 CTTCGTTACGGCATTAAGCCCTCTCTTGAGTCCCATGAATGAAGAACTGAAGCTGG 975
QY 372 LuThrLeuValValValAspLysLysMetMetGlnAsnHisGlyHisGlyAsnHisThr 392
DB 976 AGACCTTGTTGGTGGTGGCGCAAAAGATAGTGAAGAAACATGCGCATGAATATACCA 1035
QY 392 hTyrValLeuThrHisLeuAsnMetValSerAlaLeuPheLysAsp----- 407
DB 1036 CTTACGTCGTCACGATATCAACATGATCTGCTTATTCAGAGTGAAGAAATAGAG 1095
QY 407 ----- 407
DB 1096 GAAACATCAACATTCGATTTGATGCTGATTTCTTAAGATGAACAGCCAGACTGG 1155
QY 408 -----GlyLeuM 410
DB 1156 TGATAAGTACCAACGAGACCAACCTTAAGTAGCTTCTGCAAGTGGCACTGCGATTTGA 1215
QY 410 eGClYysAspGlyYThrArgHisAspHisAlaHisLeuLeuThrGlyLysAspHisCys 430
DB 1216 TGGGAAAGATGGAGCTGTCATGACCAAGCCATCTTACTGACTGGTCTGGATATAGTT 1275
QY 430 eTrrLysAsnGluProCyAspThrLeuGlyPheAlaProLysSerGlyMetCysSerL 450
DB 1276 CTTGGAAGATGAGCCCTGTGACACTTTGGATTTCACCCATTAAGTGAATGTGTAGTA 1335
QY 450 YGlyTrArgSerCyThrHisAsnGluAspThrGlyLeuGlyLeuAlaPheThrHisAlaH 470
DB 1336 AATATGCAAGCTGCAAGATTAAATGAAGATACAGGCTTGTGAAGCTGACCATTTGCC 1395
QY 470 iGluSerGlyHisAsnPheGlyMetHisHisAspGlyGluGlyAsnMetCyValLys 490
DB 1396 ATGAGCTTGACACCAACTTTGGCATGATTCATGATGAAGAGAAACATGCTGAAGAA 1455
QY 490 eGluGlyValnHisLeuMetSerProThrLeuAlaGlyYArgAsnGlyValPheSerTrrSer 510
DB 1456 CCGAGGGAACATCATGTCCTCCCTACATTGGCAGAGCAATGAGACTTCTCTGCTGTCAC 1515
QY 510 rCySerArgGlnTyrLeuHisLysPheLeuSerThrAlaGlnAlaHisCysValLeuAla 530
DB 1516 CCGCAGCGCGAGTATACACAAATTTCTAAGCACCGCTCAAGCTATCTGCTGCTG 1575
QY 530 sPGLnProLysProValLysGlyYThrLysTyrProGluLysLeuProGlyGluLeuTyr 550
DB 1576 ATCAGCAAGGCTGTGAAGGAATACAAATATCTGAGAAATTTGCCAGAGAAATATATAG 1635
```

QY 550 spAlaSerThrGlnCySlySTpGlnPheGlyGluValAlaValLeuCyMetLeuAsp 570  
DB 1636 ATGCAGAACACACAGTCAAGTGCAGTTCGAGAGAAAGCCAGCTCGATCTGAGACT 1695  
QY 570 helYsYsAspIleCySlyAlaLeuTrpCySerIleGlyArgYsCySgluThrL 590  
DB 1696 TTTAAAGAGACATCTTAAAGCCCTGTGTCATGTATTGAGAAAGAAATGTGACCTA 1755  
QY 590 yAsPheMetProAlaAlaGluGlyThrIleCySglYsHsAspMetTrpCySargIYglYg 610  
DB 1756 AATTATGCGACGACGAGAAAGGACACATTTGTGGCATGATCATGTGTGCGGGAGAGAC 1815  
QY 610 lncYsVallySTpYrgYAspGluGlyProlyProthrhIseGlyHsIleSTpSerAspTrs 630  
DB 1816 AGTGTGTGAATATGTGTGATGAAGGCCCAAGCCCACTGAGCCACTGTGCTGACTGT 1875  
QY 630 eSerTrpSerProCySsErArgThCySglYglYglYValIseHsIleSargSerArgLeuc 650  
DB 1876 CTTCCTTGTCCTCCATCTCCAGACCTGCGAGGGGAGATATCTCATAGAGTCCGCTCT 1935  
QY 650 ySThrAnProlYsProSerHsIseGlyYsPheCySgluglySerThArgThrLeuL 670  
DB 1936 GCACCAACCCCAAGCCATGCATGAGGGAAAGTTCTGTGAGGGCTCCACTCGACCTGA 1995  
QY 670 yAlaucCyAsnsErGlnlyCySProArgAspSerValAspPheAlaAlaIleGlnCyA 690  
DB 1996 AGCTCTGCAACAGTCAAGAAATGTCCTCCGGGACAGTGTGACTTCCGTGCTCACTGT 2055  
QY 690 lAGlunHsAsnsErArgArgPheArgGlyYArgHsIleYrlySTpYsProYrThrGlnV 710  
DB 2056 CCGAGACACACAGACACATTCAGAGGGGCGACCTACAGTGAAGCCCTTACACTCAAG 2115  
QY 710 aGluAspGlnAspLeuCySlyLeuYrCySIIleAGluGlyPheAspPhePheS 730  
DB 2116 TAGAAGATCAGACCTTATCAAACTCTAGTATCCAGAGAGATTGATTCTCTCTTT 2175  
QY 730 eTleuSerEnlySVallyAspGlyYrThrProCySsErGlnAspSerAlaGlnValCyS 750  
DB 2176 CTTTGTCAATTAAGTCAAGATGAGGATCTCATGCTCGAGAGATACCCCTTAATGTTTGA 2235  
QY 750 lAspPylIleCySgluArgValGlyCySAspAsnValLeuGlySsErAspAlaValAGluA 770  
DB 2236 TTAGTGGGATATCTGAGAGAGTGGATGTGACATCTCTTGATGTGATGCTGTTGAAG 2295  
QY 770 sPValCySglYValCySAsnGlyAsnAsnSerAlaCySthrlIleHsIleArgIYleuYrT 790  
DB 2296 ACGTCTGCTGGGGGTGTAAACGGGAATPAACTCAGCTGACAGATTCAACAGGGGTCTACA 2355  
QY 790 hTlyeHsIleHsIleThraEngInYrYrThHsIleMetValThrlleProSerGlyAlaArgS 810  
DB 2356 CCAAGCACACACACACAGATATTATCACATGGTCAACATCTCTTGTGAGCCCGGA 2415  
QY 810 eXlleArgIleYrglUmeAsnValSerThSerYrIleSerValArgAsnAlaLeuA 830  
DB 2416 GATCCGATCTATGAATGAAGCTCTTAACTCCCTCAATTTCTGCGCCCATGCCCTTA 2475  
QY 830 xSArgYrYrYrLeuAsnGlyHsIleSTpThrValAspTrpProGlyArgYrYrlySsPheSerg 850  
DB 2476 GAAGGTACTACCTGAACTGGGACCTGGACCTGGGACCTGGGCGGTCAAAATTTTCGG 2535  
QY 850 lYrThThrPheAspYrYrArgArgSerYrYrAsnGlnProGluAsnLeuIleAlaTrnGlyP 870  
DB 2536 GCACTACTTTCATCAACACAGGTCTTATTAATGAGCCCAAGAACTTAACTGACTACGAGC 2595  
QY 870 rOThrAsnGlnThrLeuIleValAGluLeuPheGlnGlyArgAsnProGlyValAlaIleT 890  
DB 2596 CAACCAACAGACACATGTTGTGAGCTCTGTTTCAAGGAGAAAGAAACCCGGGTGTTGCT 2655  
QY 890 rpglutySerMetProArgLeuGlyYrThGlnlySgluProProAlaGlnProSerYrT 910  
DB 2656 GGGAACTACTCAATGCTCTGCTGGGAGCCGAGAAAGAGCCCTGCGCCCAAGCTACA 2715  
QY 910 hTTPAlaIleValArgSerGluCySsErValSerCySglYglYglYArg 926

DB 2716 CTTGGGCATCGTGCCTCTGAGTCTCGTCTCGGAGGGAGACAG 2765  
RESULT 4  
US-10-217-774-5  
Sequence 5, Application US/10217774  
Patent No. 6734007  
GENERAL INFORMATION:  
APPLICANT: Carl Johan  
APPLICANT: Fridde, Erin  
TITLE OF INVENTION: No. 6734007el Human Proteases and Polynucleotides Encoding the  
FILE REFERENCE: Lex-0219-USA  
CURRENT APPLICATION NUMBER: US/10/217,774  
PRIOR FILING DATE: 2002-08-12  
PRIOR APPLICATION NUMBER: US/09/930,872  
PRIOR FILING DATE: 2001-08-14  
PRIOR APPLICATION NUMBER: US 60/225,852  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 4042  
TYPE: DNA  
ORGANISM: homo sapiens  
US-10-217-774-5  
Alignment Scores:  
Pred. No.: 0 Length: 4042  
Score: 3981.50 Matches: 764  
Percent Similarity: 78.26% Conservative: 17  
Best Local Similarity: 76.55% Mismatches: 38  
Query Match: 76.04% Indels: 181  
DB: 4 Gaps: 10  
US-09-981-151D-8 (1-952) x US-10-217-774-5 (1-4042)  
QY 1 MetLysProArgAlaArgGlyYrPArgGlyLeuAlaAlaLeuTrpMetLeuAlaGln 20  
DB 99 ATGAAGCCCGCGCGCGGATGCGGGCTTGGCGCGCTGTGATGCTGCTGCGCGAG 158  
QY 21 ValAlaGluGlnValSerProGlyArgSerHsIseGlnAGlyAsnHsArgIYserGlyGln 40  
DB 159 GTGGCGAGCA----- 169  
QY 41 LeuGluAlaSerProArgLeuLeuSerArgIYProArgArgLeuThrAlaMetSer 60  
DB 169 ----- 169  
QY 61 ProLeuPheSerAlaGlyYrThCySValArgHsIseGlyYrThArgSerGlySerAlaTrpGlu 80  
DB 170 -----GGCACCTGCTGCGCCATGGGACCCACAGCGGACGCGCTGGGAG 214  
QY 81 ProGluArgProAlaSerSerSerThrArgGlyAlaAlaGlyLeuAspGlyYrlySglYAr 100  
DB 215 CCCGAGCTCCCGGCTCTCTCCACCCGCGAGGCGCGGCTGAGTGAAGAAAGGCG-- 272  
QY 100 gAspMetAspGluAlaGlyAsnHsIleSargSerGlnGlnThraSerThrGlyYrThGluAsnG 120  
DB 272 ----- 272  
QY 120 nThrLeuHsIleValLeuThrGlnYrYrAspLeuValSerAlaYrGluValAspHsIleArgG 140  
DB 273 -----GAATATGACCTGCTCTCTCTCAACGAGTTTGAACACAGGGG 313  
QY 140 yAspYrValSerHsIseGlnIleMetHsIleGlyArgArgArgArgAlaValAlaIle 160  
DB 314 CGATTACGTGTCCCATGAATCATGACCATCAGCGGCGGAGAAAGACAGTGGCTGTCT 373  
QY 160 rgluValGluSerLeuHsIleLeuArgLeuYsGlyYrProArgHsAspPheHsIleMetAspLe 180  
DB 374 CGAGGTTGAGTCTTCTTCACTTCCGCTGAAGAGCTCCAGGACACACTTCCACGTGATCT 433

QY 180 uatgthrserSerleuVal1aProglyphe1leVal1aGlnThrleuGlyThrG1 200  
 DB 434 GAGGACTTCCAGCAGCTTACTGGCTCTGCTTATTGTGACAGCGTTGGAAAGACAG 493  
 QY 200 ythrlyserVal1aGlnThrleuProProGluAaspheCyphetYrGlnGlySerleuAr 220  
 DB 494 CACTAAGTCTGTCAAGCTTTACCGCCAGAGACTTCTGTTCTATCAAGGCTTTGCG 553  
 QY 220 gserH1sarGAsnSerProserH1sGlyGlyPheCyseGluGlySerThrArGThre 240  
 DB 554 ATACACAGAAATCC---TCACTGGGCCCTTTCACTGCCAAGGCTTGTCAAGCATGAT 610  
 QY 240 ulysleuCyAAsnserGlnlyserCyProArGAspSerValAspPheArG1a1aGlnCy 260  
 DB 611 ACCA-----ACAGAAAGGCGAGATTACTTCTTAAGGCGACT 646  
 QY 260 ba1aGluH1aAsnSerArGArGpheArG1yArG1sTrYleTrlyPProfYrThrG1 280  
 DB 647 TCCTTCACACCTCTCA-----TGGAA----- 668  
 QY 280 nValGlu1aAspLeuCylysleuTyryCySile-1a1aGluGlyPheAspPhePheS 300  
 DB 669 -----CTCGCAGAG----- 678  
 QY 300 erleuSerAnlyVallyAspGlyThrProCyserGluAAspSerArGAsnValCyS1 320  
 DB 679 --CTGGCCAAAGGAGGCTCGCCATCCCACTGATCAAGAGATTCACAAAGGCCCATGC 736  
 QY 320 1aAspGly1leCyseGluLeuSerValysSerThSer-----AlaHis----- 334  
 DB 737 TCCT-GGGGCCAGTGAAGTCTGTGACCTCAAGGACATGGAGCTGGCACATCAACCC 795  
 QY 334 ----- 334  
 DB 796 TGCACAGCAGCAGCTTCGCCCTGGAGCTGCCAAGAAAGCATTTCTGTGAAGACGA 855  
 QY 335 -----MetProGlnProProlyseGluAAspLeuPhe1leuProAspGlyTyrylys 352  
 DB 856 AGAATATACATGCCCGAGCCCTCCAAAGGAAGACCTTTTCATCTTGCCAGAGATTAAGT 915  
 QY 352 erCyaleuArG1slyArGserleuLeuArGserH1aArGAsnGluGluLeuAsnValG 372  
 DB 916 CTTCCTTAAGCGCATTAAGCGCTCTCTCTGAGGTCCCATAGAAATGAAGACTGAAGCTG 975  
 QY 372 1aThrleuVal1aValAspLyseMeMetGlnAsnH1sGlyH1sGlyAsn1leGThT 392  
 DB 976 AGACCTTGTTGGTGTGATGACAAAGATGATGCAAAACATGGCCATGAAATATATCCA 1035  
 QY 392 hTrTyValleuThr1leleuAsnMetValSer1a1euphe1ysAsp----- 407  
 DB 1036 CCAAGCGTCAAGATTAATCAATGATCTGCTTATTCAAAAGATGGAACAATAGAG 1095  
 QY 407 ----- 407  
 DB 1096 GAAACATCAACATTGCAATTGTAGTCTGATTTCTAGAAAGATGAACAGCCAGACTGG 1155  
 QY 408 -----GlyLeuM 410  
 DB 1156 TGAATAGTCAACAGCAGACACACCTTAAGTAGCTTGGCCAGTGGAGCTGAGATGA 1215  
 QY 410 ecGlylyAspGlyThrArG1sAspH1sAla1leleuLeuThrGlyLeuAsp1leCyS 430  
 DB 1216 TGGGGAAGATGGGACTCGTCATGACCAAGCCCATTTACTGATGCTGTGAGATATATGTT 1275  
 QY 430 erTrlyAsnGluProCyAspThrleuGlyPheAlaPro1leserGlyMetCyser1 450  
 DB 1276 CCGGAGAGATGAGCCCTGTGACACTTGGGATTTGACCATTAAGTGGATGTGATGTA 1335  
 QY 450 yTrTyArGserCyThr1leAsnGluAspThrGlyleuGlyleuAlaPheThr1la1aH 470  
 DB 1336 AATATGCAAGCTCAAGATTAATGAAGATACAGGCTCTGAGCTGGCCCTTACCATTTGCC 1395  
 QY 470 1aGluSerGlyH1aAsnPheGlyMet1leH1sAspGlyGluGlyAsnMetCylysleys 490

DB 1396 ATGAGTCTGACACACACTTTGGCATGATCATGATGAAAGGAGACATGTGTAAGTA 1455  
 QY 490 ecGluGlyAsn1leMetSerProThrleuAlaGlyArGAsnGlyVal1PheSerTrpSerP 510  
 DB 1456 CCGAGGCAACATCATGTCCTCCATCACTGTGACAGAGCAATGAGTCTTCTCTGTGTAC 1515  
 QY 510 roCyserArGlnTyryleuH1slyPheLeuSerThra1aGlnAla1leCyaleu1a 530  
 DB 1516 CCGCAGCCGCGCAGATCTCAACAAATTTCTAAGCACCCCTCAAGCTATCTGCTTGCTG 1575  
 QY 530 pGlnProlypProVallyseGlyTyryleTyryProGluLyseuProGlyGluLeuTyra 550  
 DB 1576 ATCAGCCAAAGCCTGTGAAGAAATACAAATATCTGAAGAAATTGCAGAGAAATTAATG 1635  
 QY 550 sPAlaAsnThrGlnCylysTrpGlnPheGlyGluLyAs1a1ysleuCyMetLeuAsp 570  
 DB 1636 ATGCAAACACACAGTGCAGAGTGGCAGTGGAGAGAAACCAAGCTTCATGCTGACT 1695  
 QY 570 helyslyAsp1leCylysAla1eUTrpCyH1sArG1leGlyArGlyCyseGlyUThT 590  
 DB 1696 TTTAAAGACATCTTAAGCCCTGTGTCATGCTATTTGAAGAAATGGAACATRA 1755  
 QY 590 ySPheMetProAla1aGluGlyThr1leCyseGlyH1sAspMetTrpCyArG1yGlyG 610  
 DB 1756 AATTATGCAGCAGCAGAGAGACAAATTTGTGGCATGACATGTGTGCCGGGAGAGAC 1815  
 QY 610 1ncysVallyserTyryleAspGluGlyProlypProThrH1sGlyH1sTrpSerAspTrS 630  
 DB 1816 AGGTGTGAATATGTGTATGAAGGCCCAAGCCCAAGTGGCCCATGTGTGGACTGTG 1875  
 QY 630 erSerTrpSerProCyserArGThrCyseGlyGlyGlyValysSerH1sArGserArGLeu 650  
 DB 1876 CTTCTTGTCCTCCATCTTCAGGACTGCGGAGGGGAGATATCTCATAGAGTGGCTCT 1935  
 QY 650 ySPheAnProlypProserH1sGlyGlylyPheCyseGluGlySerThrArGThrleu 670  
 DB 1936 GCACCAACCCCAAGCCTGATGAGAGGAGATTTGTGAGGGCTCCATCGCACCTGTA 1995  
 QY 670 yAleuCyAsnserGlnlyserCyProArGAspSerValAspPheArG1a1aGlnCyA 690  
 DB 1996 AGCTTGCAACAGTCAAGAAATGCCCCGGGACAGTGTTCATCTCGTGTCCAGTGTG 2055  
 QY 690 1aGluH1sAsnSerArGArGpheArG1yArG1sTrYrlyserTrlyPProfYrThG1y 710  
 DB 2056 CCGAGCAACACAGCAGACATTCAGAGGCGGCACTCAAGTGAAGCTTACACTCAAG 2115  
 QY 710 a1GluAspGlnAspLeuCylysleuTyryCyS1le1a1aGluGlyPheAspPhePheS 730  
 DB 2116 TGAAGATCAGGACTTATGCAACTCTACTATGCAAGAGATTGATTTCTCTTT 2175  
 QY 730 erleuSerAnlyVallyAspGlyThrProCyserGluAAspSerArGAsnValCyS1 750  
 DB 2176 CTTTGCAATTAAGTCAAGATGGGACTCATGTCCGAGAGATACCCGTAAATGTTTGA 2235  
 QY 750 1aAspGly1leCyseGluArGVal1GlyCyAspAsnValleuGlyserAspAla1aGluA 770  
 DB 2236 TGAATGGATATGTGAAGAGTTGATGACAAATCTTGGATTTGATGCTGTTGAAG 2295  
 QY 770 sPValCyseGlyValCyAsnGlyAsnAsnSerAlaCySerH1leH1sArG1yLeuTyT 790  
 DB 2296 ACGTGTGGGGGTGTAAACGGGAATTACTCAAGCTGCAGCATTCACAGGGGTCTTACA 2355  
 QY 790 hTrlyH1sH1sH1sThraAsnGlnTyryThH1sMetVal1Thr1leProserGlyAlaArS 810  
 DB 2356 CCAAGCACACACACCAACAGTATTAACATGTGTCAACATTCCTTGTGAGCCCGGA 2415  
 QY 810 er1leArG1leTyryGluMetAsnValserThSerTyry1leserValaArGAsnAlaLeu 830  
 DB 2416 GTATCGCATCTATGAAGAAAGTCTTACTCTCACTTCTGTGCGCAATGCCCTTA 2475  
 QY 830 rGArGTyryrleuAsnGlyH1sTrpThrValAspTrpProGlyArGlylyPheSerG 850

Db 2476 GAAGTACTACTGGAATGGGCACTGACCGTGGACCTGGCCCGCGGTACCAATTTTCG 2535  
Qy 850 |YThrThrPheArgPyrArgArgSerTyraAngluProgluAenluAilaThrGlyP 870  
Db 2536 GCACACTTTCGACTACAGACGGCTCTATATAGCCCGAGAACTTAATCGCTACTGGAC 2595  
Qy 870 |roThraAngluThrTrluAilaValGluLeuLeuPheGlnGlyArgAnProgluValAlaIst 890  
Db 2596 CAACCAACGAGACACTGATTGTGAGCTGCTGTTTCAGGAGAGAACCCCGGTGTGCT 2655  
Qy 890 |rogluTySerMetProArgLeuGlyThrGluArgInProProAlaGlnProSerTyrt 910  
Db 2656 GGGAAATACTCANCGCTCGCTTGGGACCGAAGAACGCCCTGCCACGCCAAGCTTAC 2715  
Qy 910 |hTrpAlaIleValArgSerGluCysSerValSerCysGlyGlyArg 926  
Db 2716 CTGGGCACTCGCGCTCGTGAAGTCTCGGTGCTCGGAGGGGAGACAG 2765  
RESULT 5  
US-09-930-872-1  
/ Sequence 1, Application US/0930872  
/ Patent No. 6448388  
/ GENERAL INFORMATION:  
/ APPLICANT: Fridde, Carl Johan  
/ APPLICANT: Hilbun, Erin  
/ TITLE OF INVENTION: No. 6448388el Human Proteases and Polynucleotides Encoding the Se  
/ FILE REFERENCE: LEX-0219-USA  
/ CURRENT APPLICATION NUMBER: US/09/930,872  
/ PRIOR FILING DATE: 2001-08-14  
/ PRIOR APPLICATION NUMBER: US 60/225,852  
/ PRIOR FILING DATE: 2000-08-16  
/ NUMBER OF SEQ ID NOS: 5  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 1  
/ LENGTH: 1476  
/ TYPE: DNA  
/ ORGANISM: homo sapiens  
US-09-930-872-1  
Alignment Scores:  
Pred. No.: 3,31e-146 Length: 1476  
Score: 1678.50 Matches: 359  
Percent Similarity: 63.26% Conservative: 138  
Best Local Similarity: 60.23% Mismatches: 40  
Query Match: 32.06% Indels: 181  
DB: 3 Gaps: 10  
US-09-981-151d-8 (1-952) x US-09-930-872-1 (1-1476)  
Qy 1 MellyrProArgAlaArgGlyTTPArgGlyLeuAlaAlaLeuTTPMetLeuLeuAlaGln 20  
Db 1 ATGAAGCCCCCGCGCGCGATGGCGGGCTTGGCGCGCTGTGATGCTGTGGCGCAG 60  
Qy 21 ValAlaGluGlnValSerProGlyArgSerHnIsglnArgGlyAsnArgGlySerGlyGln 40  
Db 61 GTGGCGGAGCA----- 71  
Qy 41 LeuGluAlaSerProProArgLeuLeuSerArgGlyProArgArgLeuThraIaMetSer 60  
Db 71 ----- 71  
Qy 61 ProLeuPheSerAlaGlyThrCysValaArgHnIsglyThrArgSerGlySerAlaTTPGlu 80  
Db 72 -----GGCACTGTGCGTGTGCGCATGGAGCCCGAGCGCGCGCTGTGGAG 116  
Qy 81 ProGluArgProAlaSerSerSerThraArgGlyAlaAlaGlyLeuAspGly-LysGlyYAr 100  
Db 117 CCCGAGCGTCCCGCGCTCTCTCCACCGCGAGCGCGCGCGCTGTGATGAAAAGGCG-- 174  
Qy 100 gAepMetAepGluAlaGlyAsnHnIsgSerGlnGlnThraAnThrGlyThrGluAsnG 120  
Db 174 ----- 174

Qy 120 nThrLeuHnIsvAlleuThrGlnTyrAspLeuValSerAlaTyrgluValAspHnIsgArg 140  
Db 175 -----GAATATGACCTGTCTCTGTCTTACGAGTTGACACAGCGGG 215  
Qy 140 YAsPyrValaSerHnIsgluIleMetHnIsglnArgArgArgAlaValaIaIaSe 160  
Db 216 CGATTACGTGTCTCCATGAATATCATCACATACGGCGGAGAAAGACAGTGGCGGTGTC 275  
Qy 160 rGluValGluSerLeuHnIsvLeuArgLeuLysGlyProArgHnIsvAspPheHnIsvAspLe 180  
Db 276 CGAGGTGAGTGTCTTACCTTCGCGCTGAAAGCTCCAGGACGACCTTCCAGTGTGATCT 335  
Qy 180 YArgThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrG 200  
Db 336 GAGGACTTCAGACACCTTATGTGCTTCGCTTATTTGTGACAGAGCTTGGGAAAGCAG 395  
Qy 200 YThrIysSerValGlnThrLeuProProGluAspPheCysPheTyrglnGlySerLeuAr 220  
Db 396 CACTAAGTCTGTGACAGACTTTCACCGCAGAGGACTTCTGTTTCTATCAAGGCTCTTTGCG 455  
Qy 220 gSerHnIsvArgAnSerProSerHnIsglyLysPheCysgluGlySerThraArgThrle 240  
Db 456 ATCACACAGAAACTCC--TCAGTGGCCCTTCAACCTGCCAAGGCTTGTCAAGCATGAT 512  
Qy 240 uLysLeuCyAsnSerGlnLysCysProArgAspSerValAspPheArgAlaIaGlnCy 260  
Db 513 ACGA-----ACAGAAAGCGAGATTACTTCTTAAGGCCACT 548  
Qy 260 sAlaGluHnIsvAnSerArgArgPheArgGlyArgHnIsvTyrlsTPlysProTyThrG 280  
Db 549 TCCTTCACACCTCTCA-----TGAAA----- 570  
Qy 280 nValGluAlaAspLeuCyLysLeuTyrcysIle-AlaGluGlyPheAspPhePhe 300  
Db 571 -----CTCGGACAGAG----- 580  
Qy 300 erLeuSerAnLysValLysAspGlyThrProCysSerGluAspSerArgAnValCysI 320  
Db 581 --CTGCCCAAGGACCTGCGCATCCACGTACTGTATCAAGAGATCCAGAGCCCCCATGC 638  
Qy 320 LeAspGlyIleCysgluLeuSerValIaSerThSer-----AlaHis----- 334  
Db 639 TCCT--GGGCGCAGTGAAGTCTCTGTGAGCTCAAGACACATGGAGCTGCACATCAACCC 697  
Qy 334 ----- 334  
Db 698 TGCACAGACGACCTTGCCTGGGACTGCCCAAAAGACAGCATTTCTGTGAAGACGCA 757  
Qy 335 -----MetProGlnProProLysGluAspLeuPheIleuProAspGlyTyrls 352  
Db 758 AGAAATACATGCCCCAGGCTCCCAAGGAAGACCTTTCATCTTGGCAATGATGATTAAGT 817  
Qy 352 erCysLeuArgHnIsvLysArgSerLeuLeuArgSerHnIsvArgAnGluGluLeuAnValG 372  
Db 818 CTTCGTTACGGCATAGGCTCTCTTGTAGGTCCTCCATGAATATAAACAATCAAGACGTGG 877  
Qy 372 LuThrLeuValValaAspLysLysMetMetGlnAsnHnIsglyHnIsgluAnIleThr 392  
Db 878 AGACCTGTGTGTGTGACAAAAAAGATGATGCAAAAACATGGCCATGAAAAATATCACCA 937  
Qy 392 hTrpValLeuThrIleuAnMetValSerAlaLeuPheLysAsp----- 407  
Db 938 CTTAGTGTCTACATCTCAACATGTATCTGCTTATTCAAAAGATGAACAATATAGAG 997  
Qy 407 ----- 407  
Db 998 GAAACATCAACATTGCAATTGTAGTCTGATTTCTTGAAGATGACAGACGACGATCG 1057  
Qy 408 -----GlyLeuM 410  
Db 1058 TGATTAAGTACACGACGACACACCTTAAGTAGCTTGCACAGTGCAGTCTGTGATTTGA 1117  
Qy 410 etGlyLysAspGlyThrArgHnIsvAspHnIsvAlaIleLeuLeuThrGlyLeuAspIleCys 430

1118 TGGGGAAGATGGACTCCGATGACCAAGCCCATCTTACTGAGTGTGATATATGTT 1177  
430 eRTPhySaAnGIuProCyAaSPThrLeuGIyPheAlaProlIeSerGIyMeCySerL 450  
1178 CCGGAAGATGAGCCCTGTGACACTTTGGATTGGACCCCATTAAGGAGATGTAGTA 1237  
450 yETyArSerCyBThrIleAaNGIuAPThrGIyLeuGIyLeuAlaPheThrIleAlaH 470  
1238 AATATGGACGCTGCACGATTAATGAAGATACAGGTCTGGACCTGGCTTACCATTCGCC 1297  
470 IeGIuSerGIyHiSaAnPheGIyMeTlleHiSaAPGIyGIuGIyAaAnMeCyAlaYls 490  
1298 ATGAGTCTGCACAACTTTGGCATGATCATGATGAGAGAGAAACATGTGTAAAAAGT 1357  
490 eRTGIuGIyAaNIleMeSerProThrLeuAlaGIyArGaNGIyValAPheSerTrSerP 510  
1358 CCGAGGCAACATCATGTCCCTTACATTTGGACAGACCAATGAGATGCTTCTCCCTGGTCA 1417  
510 rOCySeArGIyTyrLeuHIleYpHeLeuSerThraLagIn 524  
1418 CCGACGCGCCGAGTATCTTACAAATTTCTTAAGATCAGTGA 1461

RESULT 6  
US-10-217-774-1  
Sequence 1, Application US/1021774  
Patent No. 6734007  
GENERAL INFORMATION:  
APPLICANT: Fiddie, Carl Johan  
APPLICANT: Hilbun, Erin  
TITLE OF INVENTION: No. 6734007el Human Proteases and Polynucleotides Encoding the  
FILE REFERENCE: LEX-0219-USA  
CURRENT APPLICATION NUMBER: US/10/217, 774  
CURRENT FILING DATE: 2002-08-12  
PRIOR APPLICATION NUMBER: US/09/930, 872  
PRIOR FILING DATE: 2001-08-14  
PRIOR APPLICATION NUMBER: US 60/225,852  
PRIOR FILING DATE: 2000-08-16  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PaeSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1476  
TYPE: DNA  
ORGANISM: homo sapiens  
US-10-217-774-1

Alignment Scores:  
Pred. No.: 3,31e-146 Length: 1476  
Score: 1678.50 Matches: 359  
Percent Similarity: 63.26% Conservative: 18  
Best Local Similarity: 60.23% Mismatches: 40  
Query Match: 32.06% Indels: 181  
Gaps: 10

US-09-981-151d-8 (1-952) x US-10-217-774-1 (1-1476)

QY 1 MetLyPrOArGAlaArgIyTTPArGyLyLeuAlaAlaLeuTTPMeTleuLeuAlaGIn 20  
DB 1 ATGAACCCCGCGCGCGGATGGCGGGCTTGCGCGCTGTGAATGCTGTGGCGAG 60  
QY 21 ValAlaGIuGIyAlaSerProGIyArGSerHIeGIAlaGIyAaAnrGIySerGIyGIn 40  
DB 61 GTGGCCGAGCA----- 71  
QY 41 LeuGIuAlaSerProArGIyLeuLeuSerArGIyProArGIyLeuThraLamETSer 60  
DB 71 ----- 71  
QY 61 ProLeuPheSerAlaGIyThrCyValArGHIeGIyThraRSeRGIySerAlaTTPGIu 80  
DB 72 -----GGCACCTGCGTGGCCATGGAGCCGCGAGCGGCGCTGGAG 116

QY 81 ProGIuArProAlaSerSerThraRGIyAlaAlaGIyLeuAPGIy- LysGIyAr 100  
DB 117 CCGGACGTCGCCGCTCTCTTCCACCGGAGCGCGGCTGGATGGAAGAGGC-- 174  
QY 100 gArPMeArGIuAlaGIyAaAnHArSeRGIyInThraEnThrGIyThrGIuAnGI 120  
DB 174 ----- 174  
QY 120 nThrLeuHIleValLeuThrGIyTyrAPLeuValSerAlaTyrGIuValAPHIaRGI 140  
DB 175 -----GAATATGACCTGGTCTGCTTACAGAGTTCACAGGAG 215  
QY 140 yArPyTyrAlaSerHIeGIuIleMeThiSHieGIAlaRGAArgAlaValAlaYls 160  
DB 216 GATTAAGTGTCCAGAAATATGATGACATGACAGCGCGGAGAGAGAGAGAGAGAGAG 275  
QY 160 rGIuValGIuSerLeuHIleuAlaGIyLeuYsGIyProArGIyHArPheHIeMeArPle 180  
DB 276 CGAGGTGAGTCTTTCACCTTCGCTGAAAGCTTCAGAGCAGACTTCACGATGATCT 335  
QY 180 yArGTyrSerSerSerLeuValAlaProGIyPheIleValGIyThrLeuGIyLysThrGI 200  
DB 336 GAGAGCTTCAGAGAGCTTATGAGCTCTGCTTATTTGACAGACTTGGAGAGAGAG 395  
QY 200 yThrLySerValGIyThrLeuProProGIyAaSPheCySPheTyrGIyGIySerLeuAr 220  
DB 396 CACTAAGTGTGGACACTTACCGGACAGGACTTCTGTTCATCAAGGCTTTGGG 455  
QY 220 gSerHIaRGAAnSerProSerHIeGIyGIyLysPheCySGIyGIySerThraRThrie 240  
DB 456 ATCACACAGAACTCC---TCAGTGGCCCTTCAACCTCCAAAGGCTTTCAGGCAATGAT 512  
QY 240 uLySLeuCySaAnSerGIyLeuCySProArGIySerValaAPheArGIAlaLagInCy 260  
DB 513 ACAG-----ACAGAGAGGAGATTACTTCTTAAGGCCACT 548  
QY 260 sAlaGIuHIeAAnSerArGIyPheArGIyArGIyIySTyPLeuProTyrThrGI 280  
DB 549 TCCTTCACACCTCTCA-----TGAAA----- 570  
QY 280 nValGIuAlaAPLeuCyAlaLeuTyrCySile-AlaGIuGIyPheArPhePhePheS 300  
DB 571 -----CTCGGACAGAG----- 580  
QY 300 eRTLeuSerAnLyValLySaAPGIyThrProCySeRGIyAaSPSerArGAAnValCyAl 320  
DB 581 --CTGCCAAGGACGCTGCCATCCACGTAAGTTCACAAAGATCCACAGAGCCCATG 638  
QY 320 lAaSPGIyTlleCySGIuLeuSerValaIleSerThrSer-----AlaHIe----- 334  
DB 639 TCCT-GGGGCAAGTGAAGTCTGTGTAACCTCAAGACATGGAGAGCTGGACATCAACCCC 697  
QY 334 ----- 334  
DB 698 TGCACAGCAGCACTTCGCTGGAGCTGCCCAAAAGCAGCATTTCTGTGAGAGAGCA 757  
QY 335 -----MetProGIyProProLyGIuAPLeuPheIleuProArGIyTyrLys 352  
DB 758 AAGAAATACATGGCCCGAGCTCCCAAGAAAGACCTTCTTCACTTGGCAGATGAGTAAGT 817  
QY 352 eCySeuArGIyAlaYsArGSerLeuLeuArGSerHIaRGAAnGIyGIuLeuAaNGI 372  
DB 818 CTTCGTTACGGCATTAAGCGCTCTCTTGAAGTCCATGAATGAAGAACTGAAGTGG 877  
QY 372 lUThrLeuValValAlaAPLyAlaYsMeTMeTGIaAnHIeGIyHieGIuAnIleThT 392  
DB 878 AGACCTTGTGTGTGTGCGCAAAAGATGATCAAAACCATGAGCCATGAAAATATCAGCA 937  
QY 392 hTyrValLeuThrIleLeuAaAnMeTValSerAlaLeuPheYsArP 407  
DB 938 CTTACGTGTCAAGATCTCAACATGTATGTGCTTATTCAAAGATGGAACATATGAGAG 997  
QY 407 ----- 407

Db 998 GAAACATCAACATTCGATTGAGTCTGATTCTTCTAGAAAGTGAACAGCCAGACTGG 1057  
QY 408 -----GlyLeuM 410  
Db 1058 TGAATAGTCACACGACGACACACCTTAAGTAGCTTTCGCCAGTGGCACTGCGATTGA 1117  
QY 410 etGlyLyAspRgLyThrArgHIsAspHIsAlIeLeuLeuThrgLyLeuAspRLeCys 430  
Db 1118 TGGGGAAGATGGAGCTCGCATGACACGCCCATCTTACTGATGCTGGATATATGTT 1177  
QY 430 etThrLyAsnGluProCysAspThrLeuGlyPheAlaProIleSerGlyMetCysSerL 450  
Db 1178 CCGGAAGATGAGCCCTGGACACTTGGATTTCACCCCATTAAGTGAATGAAATGATGA 1237  
QY 450 yEtLyArgSerCyThrIleAsnGluAspThrgLyLeuGlyLeuAlaPheThrIleAlaH 470  
Db 1238 AATATGCAAGCTGCACGATTATGAAGATACAGSTCTTGACAGCGCTTCACCATGGCCC 1297  
QY 470 fGluSerGlyHIsAsnPheGlyMetIleHIsAspGlyGluGlyAsnMetCysLyAsLyAs 490  
Db 1298 ATGAGTCTGACACACTTGGCATGATTCATGATGAGAGGGAACATGTGTAAAGT 1357  
QY 490 etGluGlyAsnIleMetSerProThrLeuAlaGlyArgAsnGlyValIlePheSerTrpSerP 510  
Db 1358 CCGAGGCAACATCATGTCCTCACTTGCAGAGCAATGAGAGTCTTCTCGGTGCAC 1417  
QY 510 rOCySerArgGlyLyLeuHIsLyPheLeuSerThraIaGln 524  
Db 1418 CCGCAGCGCGCCAGTATCTACAAATTTCTAAGATCAGTGA 1461

RESULT 7  
US-09-963-791-1  
; Sequence 1, Application US/09663791  
; Patent No. 6649399  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Scoville, John  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6649399el Human Proteases and Polynucleotides Encoding the Sa  
; FILE REFERENCE: LEX-0105-USA  
; CURRENT APPLICATION NUMBER: US/09/963,791  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: US 60/169,769  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2727  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-963-791-1

Alignment Scores:  
Pred. No.: 7,03e-119 Length: 2727  
Score: 1390.00 Matches: 313  
Percent Similarity: 49.18 Conservative: 137  
Best Local Similarity: 34.21 Mismatches: 294  
Query Match: 26.55 Indels: 172  
DB: 4 Gaps: 25

US-09-981-151d-8 (1-952) x US-09-963-791-1 (1-2727)

QY 108 HisArgSerGlnGlnThrArgHIsAspHIsAlIeLeuLeuThrgLyLeuHIsValIleThrgGln 127  
Db 64 CATAGTACACACAGGCTTTCATACAGCTTCTCAAGAGAAATTCCTGATCTTATCTTGAAAC 123  
QY 128 TyrAspLeuValSerAlaTyrGluValAspHIsAspGlyAspTyrValSerHIsGluIle 147  
Db 124 TACAGCTACTATTCATTAAGGGTTGATCAAAATGAGCAATTTCTCAGCTTTACTGTG 183

QY 148 MetHIs-----HisGlnArgArgArgAlaVal-----AlaValSerGlu 161  
Db 184 AAAAATGATAAACACTCAAGAGAGAGAGAGATGAGACCTTATGATCCACAGCAGCA 243  
QY 162 ValGluSerLeuHIsLeuArgLeuLySerGlyProArgHIsAspPheHIsMetAspLeuArg 181  
Db 244 GATATTAAGTTATTTTAACTTTCACGCTTAAGCAAGCATTTCATCTTAACCTTGACT 303  
QY 182 ThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLyThrGlyThr 201  
Db 304 CTCACACACAGATTTTGTCCAAACATTTTACAGTGAATATGGGGGAAATGGA--- 360  
QY 202 LyServalGlnThrLeuProGlu-----AspPheCysPheTyr 215  
Db 361 -----CCCCAGGAAACATGATTTTGTAGACAACTGCTATTAC 399  
QY 216 GlnGlySerLeuArgSerHIsArgAsnSerProSerHIsGlyGlyLyPheCysGluGly 235  
Db 400 ACAGGATATTTTGCAGAGATCAACGTAGTCAACTAAAGTGGCTTTAAGCAACTGTGTGG 459  
QY 236 SerThraGlyThrLeuLyLeuCyAsnSerGlnLySProArgAspSerValAspPhe 255  
Db 460 TTGCATGCTGTATT----- 474  
QY 256 ArgAlaAlaGlnCysAlaGluHIsAsnSerArgArgPheArgGlyArgHIsTyr----- 273  
Db 475 ---GCTACGAAAGATGAGAGATATT-TATGCACTTTTAAAGATACACAGAGATTCC 530  
QY 274 -----LyEtProLyProTyrThrgInValGluAlaAspLeuCySlys 287  
Db 531 CAGCATTTTATGATTAAGAAATGGCCACC-----TCATGTAT 569  
QY 288 LeuTyrCysIleAlaGlu-----GlyPhe 295  
Db 570 TTACAAAAGTCTGCGCTTCAACAGCATCTGTATGATCACTGTCACTGTGGGTTTC 629  
QY 296 -AspPhePhePheSerLeuSerAsnLyValLyAspGlyThrPro---CysSerGluAs 314  
Db 630 GGATTTTC-----ACAAAGAGTGGCAAACTTGGTGGCTGAATGA 668  
QY 314 pSerArgAsnValCysIleAspGlyIleCysGluLeuSerValIleSerThSerAlaHIs 334  
Db 669 CACATCCACTGTCTTAT-----TCATCTCAACATTAACACACATATGCCA 716  
QY 334 sMetProGlnProProLyGluAspLeuPheIleLeuProAspGlyTyrLySserCysLe 354  
Db 717 CCAC----- 720  
QY 354 uArgHIsLyAspSerLeuLeuArgSerHIsArgAsnGluGluLeuAsnValGluThrLe 374  
Db 721 -AGACAGAAAGATCAGT-----AGCATTTGAACGTTTGTGTGAACATTT 764  
QY 374 uValIleValAspLyLySMetMetGlnAsnHIsGlyHIsGluAsnIleThrThrTyrVa 394  
Db 765 GGTAGTGGCAGCAAAATGATGATGGTGGCTTACCAGTGGCCGCAACATTGAACATTAAT 824  
QY 394 lleuThrIleLeuAsnMetValSerAlaLeuPheLyAspGlyLeuMetGly----- 411  
Db 825 TTTGAGTGTGATGAATATGTGGCAAACTTTACCGTGATTCGAGCCTAGAAAGTTGT 884  
QY 411 ----- 411  
Db 885 GAATATTAATAGTGGCCGCTTAATTTGTTCTACAGAGATGACGCCAACTTGAGATAA 944  
QY 411 ----- 411  
Db 945 CCACCATCAGACAAAGTCCCTGATAGCTTGTGAATGAGAGAAATCATCTTCTCCCA 1004  
QY 412 ---LyAspGly-----ThraArgHIsAspHIsAlaIle 422  
Db 1005 CCAAGATATGAGAAACACCATTTCCAGAAATGGGATGGCCACACAGATATATGCAGTTCT 1064













[illegible]

Db	1167	TCACCCACCAATCGCGGAAAGTCCCTTAACAGCTTCTGTAACTGGCAGAAATCCATCGTGA	1226
OY	412	-----LysAspGly---ThrArgHisAspHisAlaI	421
Db	1227	ACCAAGCGGCATGGCAATGCCATTCGACAGAAAGCGGTGGCTTAACATGACACAGACG	1286
OY	421	IeLeuLeuThrGlyLeuAspIleCysSerTrpIysAsnGluProCysAspThrIleuGlyP	441
Db	1287	TGCTCATCAACGGTATGACATCTGCATCTTACAAAGAACAAACCTTGGGACACTAAGCC	1346
OY	441	healProIleSerGlyMetCysSerIstYrAsArgSerCysThrIleAsnGluAspThrG	461
Db	1347	TGCGCCCGCGTGGCGGAATGTGTAGCGCCGAGAGAAAGCTCAGAGCTGAATAGAGACATTG	1406
OY	461	IlyLeuGlyLeuAlaPheThrIleAlaHisGluSerGlyHisAsnPheGlyMetIleHisA	481
Db	1407	GCGTGGCAACAAAGGCTTACCATTTGCCACAGAGATCGGGACACATTCGGCATGAACCATG	1466
OY	481	spGlyGluGlyAsnMetCys-----LysIlySerGluGlyAsnIleMetSerProt	498
Db	1467	ACGCGCTGGGAAACAGCTGGGGCGCCGTGTCAGAACCCAGCAACCTCATGCTCTCCC	1526
OY	498	hrlLeuAlaGlyArgAsnGlyValaPheSerTrpSerProCysSerArgGlnThrIleuHisL	518
Db	1527	ACATTTACCATGAACCAACCAACCATTCCTGTGTATCTCTGCAACCGTGACTACATCAACA	1586
OY	518	ysPheLeuSerThrAlaGlnAlaIleCysLeuAlaAspGlnProValIlyAsGluT	538
Db	1587	GCTTCTTAGACTCGGGGCTGGGGCTCTGTGCTGAACAAACGGCCC---CCAGACAGAACT	1643
OY	538	yrIlyysTYrProGluIlyLeuPheProGlyIleuLeuTYrAspAlaAsnThrGlnCysIlyeTrpG	558
Db	1644	TTGGTACCCGACAGTGGACCGGGCCAGCGCTACATGACAGATGACAAATGCGCTTTC	1703
OY	558	lnPheGlyGluIlyAlaIlyLeuLeuCysMetLeuAspPheIlyIysAspIleCysIlyAlaL	578
Db	1704	AGCATGAGTCAATCAATTCCTGACAGTGAATACGGG-----GAGGCTTCGACCGCAGC	1754
OY	578	eutTrpCysHisArgIleGlyYrAsArgCysGluThrIlyIysPheMetProAlaIleGluIyT	598
Db	1755	TGTGTGTCTGAGCAAGACAAACCGGTGTATCAACAAACAGATCCGGCCGCGAGGGCA	1814
OY	598	hrlIleCys--GlyHisAspMet-----TrpCysArgGlyGlnIlyCysValIyST	614
Db	1815	CGCTGTGCGACAGCACAACCATGACAAAGGGGTGTGCTCAAAACGGGTCTGTGTCCCT	1874
OY	614	yrGlyAspGluGlyProIlyAspThrThrHisGlyHisIstPheSerAspTrpSerTrpSerP	634
Db	1875	TTGGGTGGCGC---CCAGAGGGTGTGACGAGAGCTTGGGGCGGTGAGCTCAATGGGGCG	1931
OY	634	roCysSerArgTrpThrCysGlyGlyGlyValSerHisAsArgSerArgLeuCysThrAsnProL	654
Db	1932	ACTCGACGGGACCTGTGGCGCGCGCGGTGTCTTCTTAACTGCTACTGTGACAGCGCCCA	1991
OY	654	ysProSerHisGlyGlyIlyAsPheCysGluGlySerThrArgThrIleuIlyLeuCysAsns	674
Db	1992	GGCCACACCATGGGGGGGAGTAAGTCTGTGGGTAGAGAAAGCGGCAACCGCTCGTGCACAA	2051
OY	674	erGlnIlyCysProArgAspSerValAspPheArgAlaIleGlnCysAlaGlnHisAsns	694
Db	2052	CGGATGACTGCTCCCGCTCGCTCCAGAGACTTTCAGAGAAAGTGAAGTGTTCGAATTGGA	2111
OY	694	erAsGArgPheArgGlyYrArgHisIstYrIlySerTrpIysProTYrThrGlnValGluAspGlnA	714
Db	2112	GCATCCCTTTCGTTGGGAAATTTCAACAAGTGAAACGTAC---CGGGAGGGGGCGCTGA	2168
OY	714	spLeuCysIlyLeuTYrCysIleAlaIleGluIlyPheAspPhePhePheSerLeuSerAsnL	734
Db	2169	AGGCTGCTCGCTACGCTGCTTAAGCGGAGGCTTCAACTTCTACACGGAAGAGGGCGGAG	2228
OY	734	ysValIlyAspGlyTYrThrProCysSerGluAspSerArgAsnValCysIleAspGlyIleC	754
Db	2229	CCGTGTGTGAACGGGAGACCTGTGCGGTCAACACGGGTGAACATTTTGGTGTGATGGCCAAAT	2288

Qy	754	yvsgludgvalgIcyAeAraenValLeugIyserAerAlaValgIuAerValCyseIy	774
Db	2289	GCAAGCACTGAGGCTGCAGCCAGAGCTCGGGCTCGACTCGGAGGAGCAAGTGGCGAG	2348
Qy	774	aIcyAenGIyAraAraenSerAlaCyvThriLeuIaTgIyLeuTyThriyAenIshN	794
Db	2349	TGTGTGGCGGTGACGGCAGCTGCTCGTCCGAGACCATGAGGGGTCTTACGCCACCTCAC	2408
Qy	794	IsThraenGIyTyThriAmeValThriIeProSerGIyAlaAraSerIleaIgtIet	814
Db	2409	CTGGGGCGGGTACGAGAGATGCTGCTGGATTCCCAAGGCTCGCTCCACATCTTCATCC	2468
Qy	814	yrgIuAenValSerTherSerTyIleserAlaAraAlaIeudAraIgtTyTyL	834
Db	2469	AGAGTCTGAACCTCTCTCTCACTGACTGAGCTGGCTGAAAGAGACACAGAGTCCGTGCTG	2528
Qy	834	euaenGIyhiIeTyThriValAaTrpProGIyAraTyTyLraPheserGIyThriThrPhea	854
Db	2529	TGGAGGGGCTGCTCCGAGACCCCGACCCGACCGCTGCTGAGTGGAGCCACCTTTC	2588
Qy	854	spTyTaraGArSerTyThraenIupProGIyAraIeulIeAlaThGIyProThraenGIuT	874
Db	2589	AACCTGCACAGGGGCGACAGCAGCTCGAAGCTCGAAGCTCGGACCAATTAAATGAT	2648
Qy	874	hIleuIleValgIuIeulIeupheGInGIyAraaenProGIyValAlaTrpIuTyIserIse	894
Db	2649	CTCTCATCTGATGATGATGCTGGCGCGGACCGAGCTGCTGCTCGGCTACACGCTTCATG	2708
Qy	894	eIProAraGInGIyThraGIyusGIInProProAlaInProSerTyThriThraIaIeV	914
Db	2709	CCCC---ATGCCCCGAGACTCGTGGCCCC-----TACTCTGGACATATG	2753
Qy	914	aIArg---SerGIuCySerValSerTyvGIyGIy	925
Db	2754	CGCCTTGAGCCAAATGCTCGGCGCAAGTGTGAGCGGAT	2791

```

RESULT 11
US-09-392-184-5/c
: Sequence 5, Application US/09392184
: Patent No. 6395889
: GENERAL INFORMATION:
: APPLICANT: Robison, Keith E.
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
: TITLE OF INVENTION: PROTEASE HOMOLOGS
: FILE REFERENCE: 5800-55
: CURRENT APPLICATION NUMBER: US/09/392,184
: CURRENT FILING DATE: 1999-09-09
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 5
: LENGTH: 5357
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(5357)
: OTHER INFORMATION: repolysin (ADAM family of metalloprotease)
: NAME/KEY: misc_feature
: LOCATION: (1)..(5357)
: OTHER INFORMATION: n = A,T,C or G
: US-09-392-184-5

```

**Alignment Scores:**

Pred. No.:	6,36e-105	5337
Score:	1245.50	Matches:
Percent Similarity:	48.784	Conservative:
Best Local Similarity:	33.558	Mismatches:
Query Match:	23.794	Indels:
DB:	3	Gaps:
		32

US-09-981-151D-8 (1-952) x US-09-392-184-5 (1-5357)

QY	5	ProArgArgLeuThrAlaMetSerProLeuPheSerAlaGlyThrCysValArgHisGly	72
Db	5357	CCNAAGGAAATAGACTGTGGCGGCGCC-----GGTTCCTGC-----CATGCC	531
QY	73	ThrArgSerGlySerAlaTrpGluProGluArgProAlaSerSerSerThrArgGlyAla	92
Db	5315	CGGCGGCCCCAGTCC-----CCGAGGCCCGCGCTTTGCTGCGGCCCTCTCTCT	526
QY	93	AlaGlyLeuAerGlyLyGlyAlaArgPheMetArgGluAlaGlyAsnHisIleArgSerGln---	111
Db	5264	GCTCCCTGTG-----CGCTCGGTCTCCGGGCGCCCGGAGACC	522
QY	112	GlnThrPheThr--GlyThrGluAsnGlnThrLeuHisValLeuThrGlnTrpAspLeuVal	131
Db	5228	CGACCCAGAGCTGTGCACCGAGGGCGCG-----GGCGCATGTGACATCTGT	518
QY	131	LSerAlaTrpGluValaAspHisArgGlyAspTrpValSerHisGlnIleMetHisIleGly	151
Db	5183	GCACCCGGTTCGATGCAGCGGGGGGGCTCTCTCTGTCTTAAGAGCTGTGGCCCGCCGC	512
QY	151	naArgArgArgArgAlaValaAlaValaSerGluValaGluSerLeuHisIleLeuArgLeuGly	171
Db	5123	ACTGGGCAAGGGGAGTATGTCTGTGGCCGAGAGCGCGCCGCTTTCAGACTACATAA	506
QY	171	YProArgHisAspPheHisMetAspLeuArgThrSerSerSer--LeuValAlaProGlyP	191
Db	5063	CCGCGGGCGCAGGCTCGCTTCAACCTGACCGCCATCAAGACATGCTGTGGCGCCGCT	500
QY	191	heIleValGlnThrLeuGlyLysThrGlyThrLysSerValGlnThrLeuProProGluAla	211
Db	5003	TTTGTAAGGAACCGCGGCGCGCGCGGCGCTGTGGCGCCGCGACATCCGGGCCACACCC	494
QY	211	sPheCysPheTrpGlnGlySerLeuArgSerHisArgAsnSerProSerHisGlyGly-	230
Db	4943	CGGCTGCGACCTGCTGGTGGCAGGGG-----CAGAGACCTGAGTCGAGGGTGGCC	489
QY	231	-----LysPheCysGlnGlySerThrArgThrLeuLysLeuCysAsnSerGlnL	247
Db	4892	TGGCGGCCCATCAGCGGCTGTGCACCGCTCGAAGGATGTTCCAGCTCTCCAAACGAGACT	483
QY	247	yS-Cys-----ProArgAspSerValaAspPheArgAlaAlaGlnCysAlaGlnHis---	263
Db	4832	ACTTCATTAGACCCCTGTGACAGTGTGCCCGCGCGCGCTGTGGCCACGCCAGCCCATGTGG	477
QY	264	-----AsnSerArgArgPheArgGlyValArgHisTrpLysTrpLysProTrpThrGlnVal	281
Db	4772	TGTACAGCGTCACAGCCCCCGGAGAGGCTGCGACAGCGGGGTATTCAGTGTCCAGAGA	471
QY	282	GluAlaAspLeuCysLysLeuTrpCysIleAlaGluGlyPheAspPhePheSerLeu	301
Db	4712	CCTGTGGAG--TGCAAG-----	469
QY	302	SerAsnLysValLysAspGlyThrProCysSerGluAspSerArgAsnValCysIleLeaP	321
Db	4697	-----TGATCCCGAG-----AGCTGAGATCTCGAC	467
QY	322	GlyIleCysGluSerSerValaValSerThrSerAlaHisMetProGlnProProGlyGlu	341
Db	4673	GGG-----AGCGTTGGAGACAGCGCGACAGTGGCGCGGGGCCACGCGCTGAGG	462
QY	342	AspLeuPheIleLeuProAspGlyTrpLysSerCysLeuArgHisLysArgSerLeuLeu	361
Db	4625	CGTCTA-----CACAGCGGTCCGGTC-----	460
QY	362	ArgSerHisArgAsnGluGlnLeuAsnValGluThrLeuValValaAlaAspLysLysMet	381
Db	4604	-----ACCAAGAGAAAGTGGTGTGAGACCTGTGATGATGCTATGCCAAAG	455
QY	382	MetGlnAsnHisGlyHisGluHisGlnIleThrThrGlyValaIleuThrIleLeuAsnMetVal	401
Db	4556	GTGAGATTCACCGACACCGCCAGGTTAGAGCTATGTGCTGACATATGAACATGGTG	449
QY	402	SerAlaLeuPheLysAspGlyLeuMetGlyLys-----	412



Best Local Similarity:	31.42%	Mismatches:	317
Query Match:	23.74%	Indels:	194
DB:	4	Gaps:	24

QY	84	ProAlaSerSerSerThrxArgValAlaAlaGlyLeuAerGlyValyGValyAaGMrMetAaP	103
Db	18	CCCCCTGGCCAGATCTCTCCGCTGGGCGCTGGCCCTG---GGGCTGGGGCTCATGTTGAG	74
QY	104	GIuAlaGlyAaMhiAaRgSerGlnGlnThraGlnThGlnGluAaMhiGlnThLeuHiS	123
Db	75	GTCAACGACGCCCTTCCGGTCTCA-----GATGACCTTCTGCC	113
QY	124	ValLeuThGlnTyAaRLeuValSerAlaTyGValuAaRHiAaRgLyAaRTyVal	143
Db	114	AGTCTGGAGAGCATATAGATCGCTTCCCAACCGCGTGGACACAAAGGGGCACTGCTG	173
QY	144	SeRHiSeGluLeuLeMeChIhNiAGlnAaRGAaGValAlaValaValaSerGluValGlu	153
Db	174	GCCCTTTCGCCACCTCTCCCGAAGACAGCCCGCGGCGAAGGGGGCCACGCCAGTCC	223
QY	164	SeRLeuHiSeuAaRgLeuAaRgLyGlyProAaRHiAaRPhenHiAaMetAaRLeuAaRThSer	183
Db	234	CGGCTCTTCTACAAAGATGGCGCTCGCCACACACCACTTCTGTAACCTTACCGCGAGC	293
QY	184	SeRSeRLeuValAlaProGlyPheIleValGlnThRLeuGlyValyThRThLySer	203
Db	294	TCCGCTCTACTGGACAGGGACGCTCTCCGGAGAGTCTGAGACAGGGAGGGGCTGCTGG	353
QY	204	ValGlnThLeuProProGluAaRPhCyAaRPhTyGlnGlnLySerLeuAaRSeRHiAaRg	223
Db	354	CAGAAGACGGCGCGGCCAC-----TCCCTTACGCTGGTCACTGACATGAGGACAGGCC	407
QY	224	AaRSeR-----	225
Db	408	AGCAGCTCCCATGTGATGCATCAAGACACTGTGAGGCGCTGCACGGCGCTCATGTGGCAGAC	467
QY	226	-----ProSeRHiSeGlyGlyValyPheCyGlnGlnLySerThaRg	238
Db	468	GAGAAAGACTACTGATTGAGCCCTGCACGGTGGGCC-----AAGGTTCT-----	515
QY	239	ThRLeuLySeuCyAaRSeRGluyAaCyProAaRGAaRSeR-----ValaRPhE	255
Db	516	-----CGAAGCCCGAAGAAATGAGACACATGTGCTGTAC	551
QY	256	ArgAlaAlaGln-----CyAlaGlnHiAaRSeRArg	266
Db	552	AACGCTTCCCTCTGTGGTCACCCCACTGCACACAGCGCTGTGAGTGAAGTGAAGTGAAGAA	611
QY	267	ArgPheArgGlyAaRHiAaTyRLeuTyRLeuTyRProTyRThRGlValGluAlaAaRLeuCyS	286
Db	612	CCGTGAAGAAAGGCGGACATGTGGCTGGCGGACCTTGAAGCAACCGCGCTGACAGS-----	665
QY	287	LyAaLeuTyCyAlleAlaGlnGlyPheAaRPhRhePheSeRLeuSeRAsmLyValLyS	306
Db	666	-----CCCTGGGGAAATGAAGAACAGAG	686
QY	307	AaRGLyThRProCySeRLeuAaRSeRArgaenValCyAlleAaRGLyIleCySeGluLeu	326
Db	687	CGTGGCCAGCA-----GGCCTG-----	704
QY	327	SeRValValSeRThSerAlaHiAaMetProGlnProProLyGluAaRLeuPheIleLeu	346
Db	704	-----	704
QY	347	ProAaRGLuTyRLeuSeRCyAaLeuAaRHiLyAaRSeRLeuAaRSeRHiAaRgaen	366
Db	705	-----AAGCATGCGTCAACCCGA-----	722
QY	367	GIuGluLeuAaenValGluThRLeuValValaAaRlyValyAaMetMetGlnAaMhiAaGly	386
Db	723	---GAGCGCTACGTGGAGACCTGTGTGGTGGCTGCAAGAAAGATGGGGCTTATCAAGGG	779

[illegible]

```
QY 688 GlnCyAlaGluHisSerArgArgPheArgGlyArgHisIleTyrIleTyrProTyr 707
Db 1845 CAGTGTCTGAAATTTCACAGCATCCCTTCCGTGGAAATTCACAGTGGAAAAAGTAC 1904
QY 708 ThrGlnValGluAspGlnAspLeuCySlyLeuTyrCysIleAlaGluGlyPheAspPhe 727
Db 1905 ---CGGGAGAGGGGCGCTGAAGCGCTCGCTGCTCACTGCTGACGGAAGGCTTCACTTC 1961
QY 728 PhePheSerLeuSerLeuSerValIleAspGlyThrProCysSerLeuAspSerArgAsn 747
Db 1962 TACACGAGAGAGGGCGGCGACCGGTGTGTGACGGGACACCTGCGCTGACACAGCGTGGAC 2021
QY 748 ValCysIleAspGlyIleCysGluArgValGlyCysAspAsnValIleuGlySerAspAla 767
Db 2022 ATTGGGTGTCAGTGGCGCAATTCAGACAGCTGGGCTGGACCGAGTCTTGGGCTCCGACCTG 2081
QY 768 ValGluAspValCysGlyValCysAsnGlyAsnAsnSerAlaCysThrIleHisArgGly 787
Db 2082 CCGGAGAGACAGAGTGGCGAGTGTGTGGCGGTGACGGCAGTGCCTGGCAGACATCGAGGCG 2141
QY 788 LeuTyrThrIleHisIleHisIleThrAsnGlnTyrTyrHisMetValThrIleProSerGly 807
Db 2142 GCTTCAGCCAGCCAGCTCACCTGGGGCGGGGTACAGAGATGTGCTCGATTCGCAAAAGGC 2201
QY 808 AlaArgSerIleArgIleTyrGluMetAsnValSerThrSerTyrIleSerValArgAsn 827
Db 2202 TCCGTCAACATCTTCACTCCAGAGTCTGAACCTCTCTCACTGCTGAGCTCGGAGGGA 2261
QY 828 AlaLeuArgArgTyrTyrLeuAsnGlyHisIleTyrThrValAspTyrProGlyArgTyrLys 847
Db 2262 GACACAGAGTCCCTGCTGCTGGAGGGGCTGCCGGGACCCCCCAGCCCGCTGCTGCT 2321
QY 848 PheSerGlyThrThrPheAspTyrArgArgSerTyrAsnGluProGluAsnIleAla 867
Db 2322 CTAAGCGGAGCCCACTTTCACTCACTCAAGGGGCGACAGGCTCCAGAGCTCGAAGGC 2381
QY 868 ThrGlyProThrAsnGluThrIleValGluLeuPheGlnGlyArgAsnProGly 887
Db 2382 CTGGGACCAATTATGATCTCATCTGATGATGCTGTGCGCCGACCGAGCTGCTGCC 2441
QY 888 ValAlaIleProGlyIleSerMetProArgLeuGlyThrGluAsnProProAlaGlnPro 907
Db 2442 CTCGGCTACCGCTTCAATGCCCC---ATGCGCCGAGACTCGCTGCCCC----- 2489
QY 908 SerTyrThrThrAlaIleValAsg---SerGluCysSerValSerCysGlyGlyGly 925
Db 2490 ---TACTCTGGCACTATGGCGCCCTGACCAAGTGTCTGCCAGTGTGACGCGGT 2543

RESULT 13
US-09-981-953A-1
/ Sequence 1, Application US/09981953A
/ Patent No. 6689599
/ GENERAL INFORMATION:
/ APPLICANT: RACINE, LISA A.
/ APPLICANT: TWINE, NATALIE C.
/ APPLICANT: AGOSTINO, MICHAEL J.
/ APPLICANT: MOLTMAN, NEIL
/ APPLICANT: MORRIS, ELISABETH A.
/ TITLE OF INVENTION: NOVEL AGGRECANASE MOLECULES
/ FILE REFERENCE: 08702.0075-00000
/ CURRENT APPLICATION NUMBER: US/09/981,953A
/ PRIOR FILING DATE: 2001-10-18
/ PRIOR APPLICATION NUMBER: 60/242,317
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 3766
/ TYPE: DNA
/ ORGANISM: Unknown Organism
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism: Nucleotide
/ OTHER INFORMATION: sequence of the aggrecanase molecule
```

```
US-09-981-953A-1
Alignment Scores:
Pred. No.: 2,18e-104 Length: 3766
Score: 1237.00 Matches: 318
Percent Similarity: 44.88% Conservative: 142
Best Local Similarity: 31.02% Mismatches: 342
Query Match: 23,62% Indels: 227
DB: 4 Gaps: 27

US-09-981-151d-8 (1-952) x US-09-981-953A-1 (1-3766)
QY 19 AlAGlnValAlaGluGlnValSerProGlyArgSerHisGlnArgGlyAsnArgIleSer 38
Db 35 GCGGAGGCTCCAAAGAAAGAAACCA-----AGGCCAGAGAGAGGCCAGGTGCA 88
QY 39 GlyGlnLeuGlnAlaSerProArgLeuLeuLeuSerArgGlyProArgArgLeu-ThrAl 58
Db 89 GGGAGCAGGCGAGGAAGGATCCG-----TACAGGGGCCCAACACTACTCCACCA 139
QY 58 AMetSerProLeuPheSerAlaGlyThrCysValArgHisGlyThrArgSerGlySerAl 78
Db 140 CCGAAGCCCCCAAAAGAGACCCCGGTGATGCTCGAAGGCTGMAACAGGGAGGC----- 194
QY 78 atTgLuProGluArgProAlaSerSerSerThrArgGlyAlaAlaGlyLeuAspGlyLys 98
Db 195 -----GGCACTGTGGGGGCTGCCGCGAG-CCGGGGCT 225
QY 98 AsIyArgAspMet----- 102
Db 226 GGGGAGAGACATGTGAGACAGTGGCTGTATGGCTCCCGCTGCGCAAGATCTCCGCTGG 285
QY 103 -----AArgValAlaGlyAsnHis---ArgSerGlnGlnThrAsnThrGlyThrGlnLys 119
Db 286 CCGTGGCGCTGGGGCTGGGCTCATATGTTGAGG-TCACAGAGCCCTTCCGCT-CAAGA 343
QY 119 nGlnThrLeuHisValAlaLeuThrGlnTyrAspLeuValSerAlaTyrGluValAspHisArg 139
Db 344 TGAAGTTCCTGTCCAGTCTGGAGAGCTATGAGATCGCTTCCCGACCGGGTGGACCAAA 403
QY 139 gGlyAspTyrValSerHisGlnIleMetHisIleGlnArgArgArgAlaValAlaVala 159
Db 404 CCGGGAGACTGGGCTGCTTCCGCACTCCCGGAGGAGGAGCGCGGAGCGGGAGCG 463
QY 159 lSerGlnValGluSerLeuHisIleuArgLeuLysGlyProArgHisAspPheHisMetAs 179
Db 464 CACAGCCAGTCCCGCTTCTTACAAAGTGGCTCGGCCAGACCCAGCCACTCTCTGCTGA 523
QY 179 PheuArgThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThr 199
Db 524 CTTGACCCGACACTCCCGCTTACTGGCAGGAGCAGCTGCCGCTGGAGTACAGAGGGA 583
QY 199 rGlyThrLysSerValGlnThrLeuProGluAspPheCysPheTyrGlnGlySerIle 219
Db 584 GGGCGTGGCGCTGAGAGAGGGCGGCCGCCAC-----TGCCTTACAGCTGTCACCT 637
QY 219 LArgSerHisArgAsnSer----- 225
Db 638 GAGGCGCAGGCGACAGACTCCCATGTGACATCGACAGCACTGTGAGAGCTGACAGGCT 697
QY 226 -----ProSerHisGlyGlyLysPheCysGly 234
Db 698 GATCGTGGCAGACGAGAAAGATACCTGATTAGAGCCCTGCAAGGAGGCC-----AA 751
QY 234 uGlySerThrArgThrLeuLysLeuCysAsnSerGlnLysCysProArgAspSer----- 252
Db 752 GGGTCTCT-----CGAGACCCGAGAGAAAGTGGAC 781
QY 253 ---ValAspPheAspGlyAlaGln-----CysAlaGly 262
Db 782 ACATGTGTGACAGAGCGTCTCTGTGCTGACACCCCGCACTGACACAGCGCTGGAGT 841
QY 262 uHisAsnSerArgArgPheArgGlyArgHisIleTyrIleTyrProTyrThrGlnValGln 282
```

Db 842 GAGAGATGAGAAACCGTGGAAAGGCGCCATGATGGCTGGGACCTTGAAGCCACCGCC 901  
QY 282 ualaarpleucyalybyleuyltyrcyylleaagluylphearpharpheserleuse 302  
Db 902 TGGCAGG-----CCCTTGGG 916  
QY 302 rbanlyvvalvbarglythrprocysserleuabarserarganvalcyvllaarpl 322  
Db 917 GAATGAAACAGACCTGGCCAGCA-----CG 943  
QY 322 yllecyvgluLeuSerValValserthrseralanhsmeprcglinprolysgluas 342  
Db 944 CTG----- 947  
QY 342 pleupheileuProarplutyltyrsercyvleuarghlslyeargserleuuar 362  
Db 948 -----AACGATCGGTCAAGCG 964  
QY 362 gserhlsarvbarngluLeuabnValgluthleuvalValabarplyslysmetme 382  
Db 965 A-----GAGCGTACGTGGAGACCTGTGTGGCTGGACAAAGATGATGCT 1009  
QY 382 tgluaenhsaglyhlsagluabnlethrthrtlyrvalleuThrilleuabnmetvalse 402  
Db 1010 GCGCTATCAAGGCGCGCGGATGGACATATGCTGTGCGCATATGAACATTTGCTGC 1069  
QY 402 ralaueupheylbarglyleuMetglY----- 411  
Db 1070 CAACATTTTCCAGGACTCGAGTGGGAAGACCGTTAAATCTGTAACTGCTGCAT 1129  
QY 411 ----- 411  
Db 1130 CCTGTCAAGGAGACCAAGCCACTGTAGATCAACCAATCGCGGAAGTCCCTGGA 1189  
QY 411 ----- 411  
Db 1190 CAGCTTCTGTAAGTGCAGAAATCCATCGTGAACCAAGCGGCATGGCAATGCCATTCC 1249  
QY 412 -lybargly---ThrarhlsarphlsalalleuLeuthrglyleuaprlleCyse 430  
Db 1250 AAGGAACGGTGTGGTAAACCATGACACAGAGTGTCTATCAACGCTAATGACATCTGCAT 1309  
QY 430 rtrprrybarngluProcyabarphthrleuqlrphelaarprolleserlymetCyserly 450  
Db 1310 CTACAAAGAACAACTCTGGCGCACTAGGCTCGGCCCGGTGGGGAATGTGTAGCA 1369  
QY 450 rtyrargserythrilleasngluabarphthrlyleuglyleuAlaPheThrilleAla 470  
Db 1370 CGAGAAAGCTGCAGGCTCAATGAGCAATGGCTGGCCACAGCTTCAACATTTGCCA 1429  
QY 470 rgluserglyhlsbarphgllymetllehsarplygluglyasmetCys----- 487  
Db 1430 CAAGATCGGGACACATTCGGGATGAACATGACGCGGTGGGAAACAGCTGTGGGCGCG 1489  
QY 488 -lylsyrserygluglyasnllemetserProthrleuAlaaglyarvbarnglyValPhe 507  
Db 1490 TGGTTCGAGCCAGCCAGCACTGCTGCCACATATACATGAACCAACCAATCTCT 1549  
QY 507 rtrpserProcysserarglnlyrleuhslyrpheluserthrAlaGln-AlaIleC 527  
Db 1550 GTGGTCACTCTGCAGCGCTGACATCACTACCACTTTCTAGACTCAGGCGCTGGGCTCT 1609  
QY 527 yaleuAlaaprglnProlyrProvallyleuglylyrtyrProglulylleuProgly 547  
Db 1610 GCGTGAACACCGCGCC---CCAGACAGAGACTTTGTATCCGACAGAGGACCGGCGCC 1666  
QY 547 luleuylrtrprrybarngluabnthrlnqyalyrtrprrlphneqlyglulysalalybleuCyem 567  
Db 1667 AAGCTTACATGATGAGCAATGCCGTTTCAAGATGAGATCAATGACCTCAAGTGA 1726  
QY 567 etleuabarphelyslybarplleCyelysAlaLeuThrCysylbarglyleuArglyleu 587  
Db 587 ----- 587

Db 1727 A-ATA-----CGGAGCTTCAGAGACCTGTGTCTGACGAAGCAACCGCT 1776  
QY 587 ysgluThrlyrPheMetProAlaagluyltyrilleCys---gllyhsarMet---- 604  
Db 1777 GCATCAACAAAGCATCCCGGCGCGGAGGCGAGCTGTGGCAAGCAACCATGACAA 1836  
QY 605 -----TrCyabarglygllyglncysvallyrtyrlybarpluglyProlyrProthr 623  
Db 1837 AAGGCTGTGTCAAAACGGGTCTGTCTCCCTTGGGTGGCGC---CCAGGAGGTGG 1893  
QY 623 lsglyhlsTrpserarprtrpserTrpserProcysserarghrcyvglyglly 643  
Db 1894 ACGAGCTCGGAGGCGCGGTGACTCCATGGGAGATGACAGCCGACCTGTGGCGGCG 1953  
QY 643 alSerhlsarvbarngluLeuCythrbarProlyrProserhlsaglylyrphes 663  
Db 1954 TGTCTCTTCTAGCGGTCACTGCGACAGCCAGGCAACCATCGGGGCAATGTCTGC 2013  
QY 663 lugalserthrarghthrleuylleuCyvbarngllyrCyProarbarSerVal 683  
Db 2014 TGGGTGAAGAGGCGGACCGCTCTGCAACACGATGATGTCTCCCTGCTCCAG 2073  
QY 683 rPheargAlaAlaGlnCyvalaglyhlsbarngllyrPhearglyarghlslyr 703  
Db 2074 ACTTCAGAAAGTCAAGTGTCTTAATTTGACAGATCCCTTTCCGTGGAAATTTCTACA 2133  
QY 703 ystrprrybarngluThrlnvalgluabarplleuCyvbarnglylyrtyrilleag 723  
Db 2134 AGTGAATAACGTAC---CGGGAGGAGGCGGTGAAGCGCTGTCTGCTCAAGTCCAGCG 2190  
QY 723 lugalrphabarpheserleuSeranlyvallybarpllyrProcysser 743  
Db 2191 AAGCTTCACTTCAACAGGAGGCGGACCGGTGTGACGAGCAACCTGCTCCCTC 2250  
QY 743 lUarSerargAnvalCyvllaarglylleCyvglyArgValGlyCyabarAnval 763  
Db 2251 CAGAACGCTGACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2310  
QY 763 euglySerarplalavalgluabarpllyrlyvalCyabarnglyybarngllyrtyr 783  
Db 2311 TGGGCTCGACCTGGGAGGAGCAAGTGCAGATGTGTGGCGGTGACGAGTGGCTGCG 2370  
QY 783 hrillehsarglyleuylrthrlyrlyshlsThrbarnglylyrtyrlyshmetVal 803  
Db 2371 AGACCATGAGGCGCTTCAAGCCAGCTCACTGGGCGGCTGACAGATGCTGCT 2430  
QY 803 hrilleProserglyAlaargserillearglyleuylleuMetAsnValserThrser 823  
Db 2431 GGAATCCCAAGGCTCGCTCCACATCTTCAATCCAGATCTGAACCTCTCTCAATCACT 2490  
QY 823 lSerValargAsnAlaLeuarglyrtyrleuabnglyhlsTrpThrValarPrrp 843  
Db 2491 TGGCGTGAAGGAGACAGAGATCCCTGCTGAGAGGCGCTGCCGAGACCCCGACG 2550  
QY 843 roglyArgtyrlyrPheSerlythrThrPhearPtyrArgArgserlyrbarngluPro 863  
Db 2551 CCCACGCTGCTCTGACTGAGACCACTTTCAATCGACAGGCGGCAAGCTGCC 2610  
QY 863 lUaSerleuAlaAlthrlyrProthrbarngluThrleuAlaGluLeuLeuPheGln 883  
Db 2611 AAGGCTGGAAGCGCTGGGACCGATTAATGATCTCTATGCTCATGGTCTGGCGCGCA 2670  
QY 883 lYargbarnglyValAlaTrpglutyrSerMetProArgleuqllyrthrglysglnp 903  
Db 2671 CCGAGCTCTGCGCTCGCATCGCTCAATGCC---ATGCGCGGTGATCGCTGC 2727  
QY 903 roPrAlaGlnPrrserlyrthrTrpAlaIleValArg---SerGlnCysserValserC 922  
Db 2728 CCCCC-----TACTCTGGCAATATGCGCGCTGAGCAAGAGTCTGGCGCACT 2775  
QY 922 ysglyglly 925  
Db 2776 GTGACAGCGCT 2786



RESULT 14  
US-09-369-364A-4  
; Sequence 4, Application US/09369364A  
; Patent No. 6391610  
; GENERAL INFORMATION:  
; APPLICANT: Apte, Suneel  
; APPLICANT: Hurskainen, Tiina L.  
; APPLICANT: Hirohata, Satoshi  
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases  
; FILE REFERENCE: 26473/4007/10-30-00  
; CURRENT APPLICATION NUMBER: US/09/369,364A  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 2848  
; TYPE: DNA  
; ORGANISM: Homo sapiens ADAMTS-6  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (22)..(2601)  
; NAME/KEY: misc feature  
; LOCATION: (1369)  
; OTHER INFORMATION: n = C  
; NAME/KEY: misc feature  
; LOCATION: (1620)  
; OTHER INFORMATION: n=C  
US-09-369-364A-4

Alignment Scores:  
Pred. No.: 8.01e-103 Length: 2848  
Score: 1218.00 Matches: 290  
Percent Similarity: 45.08% Conservative: 122  
Best Local Similarity: 31.73% Mismatches: 286  
Query Match: 23.26% Indels: 218  
DB: Gaps: 21

US-09-981-151d-8 (1-952) x US-09-369-364A-4 (1-2848)

QY 108 HtArSergInGlnThrAnThrGlyThrGluAnGlnThrLeuHtSValLeuThrGln 127  
DB 85 CATAGTGCACCAAGCGCTTTCATACAGTTCACAGAGCAATTCCTGACTTATCTTGAACAC 144  
QY 128 TyrAspLeuValSerIaTyrgIuValAspHisArgGlyAspTyrgValSerHisGluIle 147  
DB 145 TACCAGCTAACTATTCCTCAATAGAGGTGATCAAAATGAGCAATTCCTGACTTACTGTG 204  
QY 148 MetHis-----HisGlnArgArgArgAlaVal-----AlaValSergIu 161  
DB 205 AAAAATGATTAACACTCAAGAGAGCGAGATGATGACCCTATTGATCCACAGCAGGCA 264  
QY 162 ValGluSerLeuHtSValArgLeuLySgIyProArGHisAspPheHtSmetAspLeuArg 181  
DB 265 GATCTCAAGTATATTTTAACTTTCACTTCAGCCTATGCGCAAGCACTTCATCTTAACCTTGACT 324  
QY 182 ThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLySthrGlyThr 201  
DB 325 CTCACACACAGATTTTGTGTCAAACATTTTACAGTAGAATATTTGGGGAAAGATGA--- 381  
QY 202 LySerValGlnThrLeuProGlu-----AspPheCysPheTyrg 215  
DB 382 -----CCCAAGTGAAACATGATTTTAAAGCAACTGTCACTTAC 420  
QY 216 GlnGlySerLeuArgSerHisArgAsnSerProSerHisGlyGlyLySphCysGlyGly 235  
DB 421 ACAGGATATTTGGACAGTCAACGATGACAACTAAAGCTTTAAGCAACTGTGTGGG 480  
QY 236 SerThrArgThrLeuLySValAsnSergIuLySAspProArgAspSerValAspPhe 255  
DB 481 TTGCATGGGTCTTAT----- 495  
QY 256 ArgAlaAlaGlnCysValGluHtSAsnSerArgArgPheArgGlyArgHisTyrg----- 273

DB 496 ---GCTACAGAAAGATGAGATATTT-TATCCAACTTTAAAGAAATACACAGAGATTC 551  
QY 274 -----LysTrPlySProTyrgThrGlnValGluAlaAspLeuCysLyS 287  
DB 552 CAAGCATTTTATGATGAAATGGCCACCC-----TCATGTTAT 590  
QY 288 LeuTyrgCysIleAlaGlu-----GlyPhe 295  
DB 591 TTACAAAAAGTCGCCCTTCAACACAGATGTGATGATCACTCATTTGGGGTTTC 650  
QY 296 AspPhePhePheSerLeuSerAsnLySValLySAsp-GlyThrProCysSergIuAspSe 315  
DB 651 GCATTTCAACAGAGTGGCAAACTTGTGGCTGAATGACACTCCACTGTTT----- 702  
QY 315 rArgAsnValCysIleAspGlyIleCysGluLeuSerValSerThSerAlaHisSme 335  
DB 703 -----CTTATTCACCTACCAAAATTAACACACACATTCACCA 740  
QY 335 tProGlnProProLySgluAspLeuPheIleLeuProAspGlyTyrgLySerCysLeuAr 355  
DB 741 C-----AG 743  
QY 355 GHisLySArgSerLeuLeuArgSerHisArgAsnGlyGluLeuAsnValGluThrLeuVa 375  
DB 744 ACAGAGAGATCAGTG-----AGCATTTGAACGGTTTGTGAGACATTTGGT 788  
QY 375 lValValAspLySValMetMetGlnAsnHtSgIyHisGluAsnIleThrThTyrgValle 395  
DB 789 AGTGGCAGCAAAATGATGTGTGGCTACCAATGGCCGCAAAAGATTAACATTCATTTAT 848  
QY 395 uThrIleLeuAsnMetValSerAlaLeuPheLySAspGlyLeuMetGly----- 411  
DB 849 GAGTGTGATGATATTTGTTGCCAACTTTACCGTGATTCAGGCTTGAAGAGTTGTGA 908  
QY 411 ----- 411  
DB 909 TATTATAGTGCCCGCTTAATTGTTCTCAGAAAGATCAGCAAACTTGAGATTAACCA 968  
QY 411 ----- 411  
DB 969 CCATGCAACAAGTCCCTGATGATCTTGTAATGGCAAAATTCCTCTCCACCA 1028  
QY 412 -LySAspGly-----ThrArgHisAspHisAlaIleLeu 423  
DB 1029 AAGTATGGAACACCATTCACGAAATGGGATGGCCACACGATTAAGCACTTCTTAT 1088  
QY 423 uThrGlyLeuAspIleCysSerTrpLySAsnGluProCysAspThrLeuGlyPheAlaPr 443  
DB 1089 TACTAGATATGATATCTGCACCTATTAATAATGACCCTGTGGAACACTGGGCTTGGCTTC 1148  
QY 443 oIleSergIyMetCysSerLySArgSerCysThrIleAsnGluAspThrGlyLeuGlu 463  
DB 1149 TGTGGCTGAATGTGTGACCTGAAGAGCTGCACATTAATGAAGACATTTGGCCCTGGG 1208  
QY 463 lYleuAlaPheThrIleAlaHisGluSergIyHisAsnPheGlyMetIleHisAspGlyGlu 483  
DB 1209 TTCAGCTTTTACCATTCACATGAGATTTGTTCACAAATTTTGTGTATGAACATGATGAAT 1268  
QY 483 uGlyAsnMetCys-----LySAspSergIu-GlyAsnIleMetSerProThrLeuAlaG 501  
DB 1269 TGGAAATTCCTGTGAGCAAGAGTCAAGAGCAACAAATTAATGAGGAGCTCACTTACAG 1328  
QY 501 lYArgAsnGlyValPheSerTrpSerProCysSerArgGlnTyrgIleuHtSlySphLeuS 521  
DB 1329 CGAATTAACCAATCCTTTTCTCGTGTGCTTGAAGTGAAGAAATACAT-CACTCACTTTT- 1386  
QY 521 eThrAlaGlnAlaIleCysLeuAlaAspGlnProLySProValLySgluTyrgLyTyrgP 541  
DB 1386 ----- 1386  
QY 541 roGluLySLeuProGlyGluLeuTyrgAspAlaAsnThrGlnCysLySTrpGlnPheGlyG 561



QY 299 eSerLeuSerAsnLysValLysAspGlyThrProCysSerGluAspSerArgAsnValCys 319  
||| : : : : :  
Db 635 -----TGTACCAG-----AGCTGAG 651  
QY 319 sIleAspGlyIleCysGluLeuSerValValSerThrSerAlaHisMetProGlnProP 339  
: : : : :  
Db 652 TCTCGACGGG-----AGCGTTGGAGACGGCGACGCG--TGGCGGGCGCCACG 698  
QY 339 oLysGluAspLeuPheIleLeuProAspGlyTyrLysSerCysLeuAspArgHisLysArgSe 359  
||| : : : : :  
Db 699 GCTGAGCGCTTA-----CAACAGCGGTC 722  
QY 359 rLeuLeuArgSerHisArgAsnGluGluLeuAsnValGluThrLeuValValAspLys 379  
: : : : :  
Db 723 GGTG-----AGCAAGAGAAAGTGGTGTGAGACCTGGTATAGTGTATGTC 767  
QY 379 sLysMetMetGlnAsnHisGlyHisGluAsnIleThrThrTyrValLeuThrIleLeuAs 399  
: : : : :  
Db 768 CAAAAATGTGTGAGTACACGACGACGCGCAGGTTGAGAGCTATGTCTGACCATCATGAA 827  
QY 399 rMetValSerAlaLeuPheLysAspGlyLeuMetGlyLys----- 412  
||| : : : : :  
Db 828 CATGTGTGGCTGGCTGTTCAATGACCCAGCATTTGGAAACCCCATTCACATCACTATTG 867  
QY 413 -----AspG1 414  
Db 888 GCGCGTGTCTGTGTGAAATGAGAGAGAGAACTTAAGATCACGACCATGACAGCA 947  
QY 414 YThr----- 415  
Db 948 CACCTTGAAAGACTTCTGCAAGTGGCAGAAAGCATCAATGAGAGGGAGATCCCATCC 1007  
QY 416 -----ArgHisAspHisAlaIleLeuLeuThrGlyLeuAspIleCysSerTrpLysAsnG1 434  
||| : : : : :  
Db 1008 CTGCAACCATGACACTGCTGCATCTGTCTACACAAAGACCTGTGTGTCAACCATGAACCG 1067  
QY 434 uProCysAspThrLeuGlyPheAlaProIleSerGlyMetCysSerLysTyrArgSerCys 454  
||| : : : : :  
Db 1068 GCCCTGTGAAACCTGTGGACTGTCCCATGTGGCGGCGATGTGCCAGCGGACGCGAGCTG 1127  
QY 454 sThrIleAsnGluAspThrGlyLeuGlyLeuAlaPheThrIleAlaHisGluSerGlyHis 474  
: : : : :  
Db 1128 CACCATCAACAGAGAGACACGGGCGCTGCGGCTTCACTGTAGCCACAGAGCTCGGGGCA 1187  
QY 474 sAsnPheGlyMetIleHisAspGlyGluGlyAsnMetCysLysLys-----SerGluG1 492  
||| : : : : :  
Db 1188 CAGTTTGGCATTCAGATGACGAGAGCGGCAATGACTGTGAGCCGTTGGGAAACGACC 1247  
QY 492 yAsnIleMetSerProThrLeuAlaGlyArgAsnGlyValPheSerTrpSerProCysSe 512  
||| : : : : :  
Db 1248 TTTTCATCATGTCTGCCAGCTCTCGTACGACGCCGCTCCCTCACTGTGTCCGCTGCAAG 1307  
QY 512 rArgGlyTyrLeuHisLysPheLeuSerThrAlaGlnAlaIleCysLeuAlaAspGlnP 532  
||| : : : : :  
Db 1308 CCGCCAGTATATGACCGGTTCTTGAACGTTGGGTGGGCTGTGGCTTGACCAACCTTCC 1367  
QY 532 o----LysProValLysGluTyrLysTyrProGluLysLeuProGlyGluLeuTyrAspAl 551  
||| : : : : :  
Db 1368 TGGCAAGGACATTATGAC-----TTCCTCGGTGCCACCTGGCTCTCTATATGATGT 1421  
QY 551 aAsnThrGlnCysLysTrpGlnPheGlyGluLysAlaLysLeuCysMetLeuAspPheLys 571  
||| : : : : :  
Db 1422 AAGCCACCAATGCGCGCTCCAGTACGGGGCTACTGTGCTTGTG-----GAGGACAT 1475  
QY 571 sLysAspIleCysLysAlaLeuTyrCysHisArgIleGlyArgLysCysGluThrLysPhe 591  
: : : : :  
Db 1476 GGAATATGTCTGCCACACACTGTGTGCT--TCTGTGGGAGCAACCTGTCACTCAAGACT 1532  
QY 591 eMetProAlaAlaGluGlyThrIleCysGlyHisAspMetTrpCysArgGlyGlyGlnCys 611  
||| : : : : :  
Db 1533 GAGTGCAGCTGTGGACGGCACCCGCTGTGGAGAAATTAAGTGTGTCTCACTGTGGAGAGTG 1592

QY 611 sValLysTyrGlyAspGluGlyProLysProThrHisGlyHisTrpSerAspTrpSerSe 631  
||| : : : : :  
Db 1593 CGTACCCGTGGGCTTCCGG-----CCGAGGCCGCGATGTGGTGTGCTGTGCTGAGCGC 1649  
QY 631 rTrpSerProCysSerArgThrCysGlyGlyGlyValLysThrHisArgSerArgLeuGlyTh 651  
: : : : :  
Db 1650 CTGTCTCATCTGTCTACGAGAGCTGTGTGCATGTGGCGTACAGAGCGCGAAGCGGACGTGCAC 1709  
QY 651 rAsnProLysProSerHisGlyGlyLysPheCysGluGlySerThrArgThrLeuLysPhe 671  
||| : : : : :  
Db 1710 GCAGCTTAGCGCCAAATACAAAGGACAGATACTGTGTGGGTAGAGCGGAACGCTCCGGCT 1769  
QY 671 uCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaAlaGlnCysAlaG1 691  
||| : : : : :  
Db 1770 CTGCAACCTGACAGGCTGCGCTGTGGCTGGCGCCCTCTTCCGACGTCAGGACGCA 1829  
QY 691 uHisAsnSerArgArgPheArgGlyArgHisTyrLysTrpLysProTyrThrGlnValG1 711  
: : : : :  
Db 1830 CTTTGAAGCTTAGCTCTTACAAAGGCGCAGCTGCACATAGGTGTCCTGTG-----GTCA 1883  
QY 711 uAspGlnAspLeuCysLysLeuTyrCysIleAlaGluGlyPheAspPhePheSerSe 731  
||| : : : : :  
Db 1884 TGAAGTGAACCCCTGTGAGCTGACATGCGCGCGCGGAGATGACTTTGCCAAGAACT 1943  
QY 731 uSerAsnLysValLysAspGlyThrProCysSerGlu-----AspSerArgAsnValCys 749  
||| : : : : :  
Db 1944 GCGGAGCGCTGTGTGATGTGGACCCCTGTGTACAGGTCCAGGTCCGAGCGGAGACCTGTG 2003  
QY 749 sIleAspGlyIleCysGluArgValGlyCysAspAsnValLeuGlySerAspAlaValG1 769  
: : : : :  
Db 2004 CATCAACGGCATCTGTGAAGACGTGGGCTGTGTGCTTGCAGATTGACTCGGTGCTATGGA 2063  
QY 769 uAspValCysGlyValCysAsnGlyAsnAsnSerAlaCysThrIleHisArgGlyLeuTyr 789  
||| : : : : :  
Db 2064 GAGCGCTGTGTGTGTGTGTCACGAGCAACGGCTCCACTGTCCACACCGTGAAGCGGACCTT 2123  
QY 789 rThrLysHisHisHisThrAsnGlnTyrHisMetValThrIleProSerGlyValAsp 809  
||| : : : : :  
Db 2124 CAGAGAGGCGCGAGGCTGTGGG-----TATGTGATGTGGGGCTGTATCCAGCGGGCCGACG 2180  
QY 809 gSerIleAlaGlyIleTyrGluMetAsnValSerThrSerTyrIleSerValArgAsnAla-- 828  
||| : : : : :  
Db 2181 CGAGATCCGCATCTCAAGAGAGTTGCCAGGCTGTGCACCTTCTGTGCACCTGCGAGCGCAGGA 2240  
QY 829 -LeuArgArgTyrTyrLeuAsnGlyHisTrpThrValAspTrpProGlyArgTyrLysPhe 848  
: : : : :  
Db 2241 CCGGAGAAAGTACTTCTCAATGT 2300  
QY 2301 GGCAGGAGACCACTTCAATACATACGACGAGGGGCAACTG3---GAGAACCTCACGTCCCC 2357  
QY 848 eSerGlyThrThrPheAspTyrArgArgSerTyrAsnGluProGluAsnLeuIleAlaThr 868  
||| : : : : :  
Db 2358 GGGTCCCAACAGAGACCTGTGTGATTCAGGTGCTGTCCCTCCGTGGCCAGCGGGG 2417  
QY 873 ----- 873  
Db 2418 GAGCAGAGCGAGATCCCAAGGCCACGACCTTCCATGGCAGGTCTGTCTGTGAGAGAT 2477  
QY 873 ----- 873  
Db 2478 GAGCCTGTGTGATGACAGAGGCTGTGTGAGCGACGCGCTCTGTGTGGCTGTAC 2537  
QY 873 ----- 873  
Db 2538 CTCAGTTTCCCATCTTTAAATGGCCCAATCTTGTAGCTGCAATTCAAGAGTGTGCTG 2597  
QY 874 -----Th 874  
Db 2598 GGGTCAAGCTCTTTAGACTGTGGGTGATGAGAGAACACCTTGTGTCTATGTGGCCCGG 2657  
QY 874 ----- 874  
Db 874 rLeuIleValGluLeuPheGlnGlyArgAsnProGlyValAlaTrpGluTyrSerMet 894

Db 2658 CCGCCACCCAGCTGCTCCAGAGAGCAACCTGGGTGCTACGATACCAAT 2717  
QY 894 cProArgLeu-----GlyThrGluYsgInProAlaGlnProSerTyrThrTrpAl 912  
Db 2718 CCACAGGAGGCGAGTGGCCACGACGAGTCCGCCG-----CCGCTGTCTCTGGCA 2771  
QY 912 aIle---ValArgSerGluCysSerValSerCysGlyGly 925  
Db 2772 TTATGGGCCCTGGACCAAGTGCAAGTCACTGCGGCAGAGT 2814

Search completed: September 10, 2005, 00:02:10  
Job time : 462 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 9, 2005, 23:27:10 ; Search time 1281 Seconds

(without alignments)  
4880.572 Million cell updates/sec

Title: US-09-981-151D-8

Perfect score: 5236

Sequence: 1 MKPRRAGMGALMMLAQ.....LEAACPSATAYTALAFLES 952

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 7351250 segs, 3289620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODE=frame+ p2n.model -DEV=xip  
-Q=/cgn2\_1/us0to.spool\_p/us09981151/runat\_07092005\_173418\_18730/app.query.fasta\_1.1095  
-DB=PublishedApplications\_NA -QFMT=fastap -SUFFIX=rmdb -MINMATCH=0.1  
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62  
-TRANS=human40.csl -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=us09981151@cgn 1.1 723 @runat\_07092005\_173418\_18730  
-NCPU=6 -ICPU=3 -NO MAP -LARGESURV -NEG SCORES=0 -WAIT -DSBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPEXT=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications\_NA:\*

1: /cgn2\_6/prodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/prodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/prodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/prodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/prodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/prodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/prodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/prodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/prodata/2/pubpna/US09\_PUBCOMB.seq:\*  
10: /cgn2\_6/prodata/2/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/prodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/prodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/prodata/2/pubpna/US10\_PUBCOMB.seq:\*  
14: /cgn2\_6/prodata/2/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/prodata/2/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/prodata/2/pubpna/US10D\_PUBCOMB.seq:\*  
17: /cgn2\_6/prodata/2/pubpna/US10E\_PUBCOMB.seq:\*  
18: /cgn2\_6/prodata/2/pubpna/US10F\_PUBCOMB.seq:\*  
19: /cgn2\_6/prodata/2/pubpna/US10G\_PUBCOMB.seq:\*  
20: /cgn2\_6/prodata/2/pubpna/US10H\_PUBCOMB.seq:\*  
21: /cgn2\_6/prodata/2/pubpna/US10I\_PUBCOMB.seq:\*  
22: /cgn2\_6/prodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
23: /cgn2\_6/prodata/2/pubpna/US11\_PUBCOMB.seq:\*  
24: /cgn2\_6/prodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
25: /cgn2\_6/prodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
26: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5236	100.0	2895	10	US-09-981-151A-7
2	5110	97.6	2997	10	US-09-981-151A-1
3	4103.5	78.4	2433	10	US-09-981-151A-3
4	3993.5	76.3	3675	17	US-10-330-176-1
5	3993.5	76.3	3675	18	US-10-275-107-16
6	3981.5	76.0	3675	13	US-10-217-774-3
7	3981.5	76.0	3675	15	US-10-296-616-1
8	3981.5	76.0	3675	21	US-10-804-457-3
9	3981.5	76.0	4042	23	US-10-217-774-5
10	3981.5	76.0	4042	21	US-10-804-457-5
11	3720	71.0	2902	10	US-09-981-151A-5
12	3291.5	62.9	4888	17	US-10-399-645-19
13	2442	46.6	3389	18	US-10-363-937-34
14	2442	46.6	3666	16	US-10-240-545A-1
15	2440	46.6	3219	18	US-10-354-983-3
16	2440	46.6	3663	18	US-10-354-983-1
17	2415.5	46.1	3445	19	US-10-391-364-86
18	2414.5	46.1	3246	19	US-10-391-364-88
19	2371.5	45.3	3630	17	US-10-161-493-123
20	2284.5	43.6	3013	14	US-10-226-560-3
21	2284.5	43.6	3013	22	US-10-990-935-3
22	2271.5	43.4	2589	14	US-10-226-560-1
23	2271.5	43.4	2589	22	US-10-990-935-1
24	2262.5	43.2	2940	17	US-10-188-186-131
25	2255	43.1	3555	17	US-10-188-186-129
26	2196.5	41.9	2805	18	US-10-275-107-18
27	2073	39.6	3954	18	US-10-354-983-5
28	1678.5	32.1	1476	13	US-10-217-774-1
29	1678.5	32.1	1476	21	US-10-804-457-1
30	1564.5	29.9	1986	18	US-10-354-983-7
31	1391	26.6	2879	9	US-09-788-043C-2
32	1390	26.5	2727	9	US-09-963-791-1
33	1390	26.5	2727	17	US-10-419-276-1
34	1390	26.5	2727	24	US-11-027-744-1
35	1385.5	26.5	2377	14	US-10-103-377C-1
36	1380.5	26.4	6565	18	US-10-467-042-22
37	1380.5	26.4	6565	24	US-11-046-868-22
38	1377.5	26.3	2052	14	US-10-103-377C-3
39	1342	25.6	1059	17	US-10-161-493-129
40	1342	25.6	1059	17	US-10-161-493-133
41	1339	25.4	1059	17	US-10-161-493-127
42	1332	25.4	1059	17	US-10-161-493-125
43	1332	25.4	1059	17	US-10-161-493-131
44	1319	25.2	2274	9	US-09-963-791-23
45	1319	25.2	2274	17	US-10-419-276-23

#### ALIGNMENTS

RESULT 1  
US-09-981-151A-7  
; Sequence 7, Application US/09981151A  
; Publication No. US20030212256A1  
; GENERAL INFORMATION:  
; APPLICANT: Edinger, Shlomit R  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: MacDougall, John R  
; APPLICANT: Malynkar, Muriel M  
; APPLICANT: Smitson, Glenda  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Peyman, John A  
; APPLICANT: Stone, David J  
; APPLICANT: Gunther, Erik  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Shinkets, Richard A

APPLICANT: Padigaru, Muralidhara  
APPLICANT: Guo, Xiaojia  
APPLICANT: Paturajan, Meera  
APPLICANT: Taupier Jr, Raymond J  
APPLICANT: Burgess, Catherine E  
APPLICANT: Zernhusen, Bryan D  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Spteck, Kimberly A  
APPLICANT: Gangolli, Esha A  
APPLICANT: Fernandes, Elma R  
APPLICANT: Gorman, Linda  
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-168  
CURRENT APPLICATION NUMBER: US/09/981,151A  
PRIOR FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 60/241,040  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,058  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,063  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,243  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/242,152  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/242,482  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,611  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,612  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,880  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/242,881  
PRIOR FILING DATE: 2000-10-24  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 2895  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-981-151A-7  
US-09-981-151D-8 (1-952) x US-09-981-151A-7 (1-2895)  
Alignment Scores:  
Pred. No.: 0 Length: 2895  
Score: 5236.00 Matches: 952  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 10

101 AspMetAspGluAlaGlyAsnHisArgSerGlnGlnThrAsnThrGlyThrGluAsnGln 120  
310 GACATGAGTGAAGCTGGAACCATCGTTCTCAGCAAACTTACACAGGAACAGAAAAACCA 369  
121 ThrLeuHisValLeuThrGlnTyrAspLeuValSerAlaTyrGluValAspHisArgGly 140  
370 ACACAGCATGTTCTCATCAATATGACCTGCTCTGCTTACAGAGTTGACACAGGGGCG 429  
141 AspTyrValSerHisGluIleMetHisHisGlnATGATGATGATGATGATGATGATGAT 160  
430 GATTACGTTCTCCATGAAATCATGACCATCAGCGGAGGAAGACATGCGCTGTTCC 489  
161 GluValGluSerLeuHisValLeuArgLeuValGlyProAlaGlnHisAspPheHisMetAspLeu 180  
490 GAGGTGAGTCTCTTCACTTCAGCTGGAAGGCCCAAGGACGATTCACATTCAGATGATCTG 549  
181 ArgThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrGly 200  
550 AGGACTTCAGACGACTAGTGCTCTGCTTATTTGTCAGACGTTGGGAAAGACAGGC 609  
201 ThrLysSerValGlnThrLeuProProGluAspPheCysPheTyrGlnGlySerLeuArg 220  
610 ACTTACGTTCTGTCAGACTTTTACCGCCAGAGACTTCTGTTTCTATCAAGGCTTTTGGCA 669  
221 SerHisArgAsnSerProSerHisGlyGlyLysPheCysGlnGlySerThrArgThrLeu 240  
670 TCACACAGAACTCCCATCCATCGCATGAGGAAAGTTCTGTGAGGGCTCCACCTGCACCTCG 729  
241 LysLeuCyAsnSerGlnLysCysProArgAspSerValAspPheArgAlaAlaGlnCys 260  
730 AAGCTCTGCAACAGCAAGAAATGTCCTCCGGGACAGTGTGACTTCGCGTCTCAGTGT 789  
261 AlaGluHisAsnSerArgArgPheArgGlyArgHisGlyLysTyrLysTyrLysProTyrThrGln 280  
790 GCCGAGCACACAGACAGATTCAGAGGGCGGACTCAAGTGAAGCTTACACTCA 849  
281 ValGluAlaSerLeuCyAspLeuTyrCysIleAlaGlnGlyPheAspPhePheSer 300  
850 GTAGAGCCGACTTATGCAAACTTACTGTATCGCAGAGGATTTGATTTCTTTTCT 909  
301 LeuSerAsnLysValLysAspGlyThrProCysSerGluAspSerArgAsnValCysIle 320  
910 TTGTCAATTAAGTAAAGATGAGCTCCATGCTCGAGGAAAGCGGTAATTTGTGTATA 969  
321 AspGlyIleCysGluLeuSerValValSerThrSerAlaHisMetProGlnProProLys 340  
970 GATGGGATATGAGACTCAGTGTGTGTCCACATCTGCGCACATGCCAGGCTCCCAAG 1029  
341 GluAspLeuPheHisLeuProAspGluTyrLysSerCysLeuArgHisLysArgSerLeu 360  
1030 GAAAGACTCTTCATCTTCCAGATGATGATTAAGTCTTCTTACCGGCATTAAGCGCTCTT 1089  
361 LeuArgSerHisArgAsnGluGluLeuAsnValGluThrLeuValValAspLysLys 380  
1090 CTGAGGTCCCATAGAAATGAAGAACTGAACGTGAGACCTTGTGTGTCACAAAAAG 1149  
381 MetMetGlnAsnHisGlyHisGluHisIleThrThrTyrValLeuThrIleLeuAsnMet 400  
1150 ATGATGCAAAACATAGGCAATGAAATATCAACACTACGTCCTCAACATCTCAACATG 1209  
401 ValSerAlaLeuPheLysAspGlyLeuMetGlyLysAspGlyThrArgHisAspHisAla 420  
1210 GTATCTGCTTATTAATCAAGATGATGATGAGGAAAGATGGAATCGTCATGACACAGCC 1269  
421 IleLeuLeuThrGlyLeuAspIleCysSerThrProLysAsnGluProCysAspThrLeuGly 440  
1270 ATCTTACTGACTGCTGTGATATATATGTTCTCGGAAGATGAGCCCTGTGACACTTTGGGA 1329  
441 PheAlaProIleSerGlyMetCysSerLysTyrArgSerCysThrIleAsnGluAspThr 460  
1330 TTTGCACCCATTAAGTGAATGTGTAAATATTCGACACTGACGATTAATGAATATCA 1389

QY 461 G1yLeuG1yLeuA1aPheThr11eAlaH1eG1uSerG1yH1aAaPheG1yMeT1eH1a 460  
DB 1390 GGCTTGAAGTGGCTTCACTTGCATGAGTCTGGAACAACCTTGGCATGATTCAT 1449  
QY 481 AaPGL1yG1uG1yAaMeT1yS1yS1eSerG1uG1yAaM1eMeT1eP1oTh1eA1a 500  
DB 1450 GAAGGAGAAAGGAAACATGTGTAAAGTCCGAGGGCAACATGTCCTTCAATGGCA 1509  
QY 501 G1yAaAaM1yA1aPheSerTPSeP1oCySeSerAaG1nTy1eH1aS1yPheLeu 520  
DB 1510 GAGAGCAATGAGATCTTCTCTGTCACCTGCAGCCGACAGATCTCAACAATTTCTA 1569  
QY 521 SerTh1aA1aG1nA1a1eCySeAaA1aAaPGL1yAaPGL1yAaG1uTy1eTy1e 540  
DB 1570 AGCAGCGCTCAACCTATCTCTGCTGATCAGCAAGCCTGGAAGAAATCAAGTAT 1629  
QY 541 ProG1u1yAaLeuProG1u1yAaLeuTy1eAaP1aAaTh1eG1nCyS1yS1eTPG1nPh1eG1y 560  
DB 1630 CTTGAGAAATGCGAGAGAAATTAATGATGAAACACAGTGCAGATGGCAGTTCCGA 1689  
QY 561 G1u1yAa1a1yAaLeuCyMeT1eAaP1e1yS1yAaP1e1yS1yAa1a1eA1aTPCyS 580  
DB 1690 GAGAAAGCCAGCTTGCATGCTGACCTTAAAGACATCTGTAAAGCCCTGTGTC 1749  
QY 581 H1aAaG11eG1yAaG1yAaG1uTh1yAaPheMeP1oA1aA1aG1uG1yTh1eCyS 600  
DB 1750 CATGATTTGGAAGAAATGAGACTTAATTTATGCGACAGACAGAAAGCCAAATTTGT 1809  
QY 601 G1yH1aAaPMeT1eTPCyAaG1yG1yG1nCyAa1yAa1yS1yG1yAaPGL1yP1o1yA 620  
DB 1810 GGGCAATGACATGTGTGCGCGGAGAGACATGTGTGAAATGTGTATGAAAGCCCAAG 1869  
QY 621 ProTh1aG1yH1a1eTPSeAaP1eTPSeSerTPSeP1oCySeSerAaG1nTy1eCyS 640  
DB 1870 CCAACCAATGGCACTGTGTGAGACTGTCTTTGCTTCCCAATGCTTCCAGACCTGCGA 1929  
QY 641 G1yG1yAa1eSerH1aAaSerAaG1eCyThAaP1o1yAaP1o1yAaP1e1yG1yAa 660  
DB 1930 GGGGAGTATCTATGAGATCGCTCTGCAACCAACCAAGCATGAGTGAAGGGAAG 1989  
QY 661 PheCyG1uG1ySerTh1aG1nTh1e1yAaLeuCyAaAaSerG1nTy1eCyS1yP1o1yAaP 680  
DB 1990 TTTCTGAGAGGCTTCACTTCCACTGCAAGCTTGCACAAAGTCAAAATCTCCCGGAC 2049  
QY 681 SerValAaP1eAaG1aA1aG1nCyAa1aG1uH1aAaSerAaG1yAaG1yAaG1yAa 700  
DB 2050 AGTGTGACTTCCGTGCTGCTGAGTGTGCGAGCAACAAGCAAGATTCAGAGGGCG 2109  
QY 701 H1a1y1e1yAaP1eP1o1yTh1eG1nA1aG1uAaPGL1aAaP1e1yAaLeuTy1eCyS 720  
DB 2110 CACTACAAGTGAAGCTTACCTCAAGTGAAGATCAGGACTTATGCAAACTCTACTGT 2169  
QY 721 11eA1G1uG1yAaAaP1eP1eP1eP1eSer1eAaSerAa1yAa1yAaPGL1yTh1eP1o 740  
DB 2170 ATGCGAAGAGATTTGATTTCTTTCTTTCTTCAAAATTAAGTCAAAAGTGGACTCCA 2229  
QY 741 CySeSerG1uAaP1eAaAaValA1aAaPGL11eCyAaG1uAaG1yAa1yCyAaAaP 760  
DB 2230 TGTCTGAGAGATGCGGTAAATGTTGTATGATGGGATATGTAAGAGTTGAGTGTGAC 2289  
QY 761 AaAa1a1e1yAaSerAaAaAa1aG1uAaP1a1CyAaG1yAa1yAaAaAaSer 780  
DB 2290 AATGCTCTTGAATCTGATGCTGTTGAAGACGTCTGTGGGTGTAAAGGAAATTAATCA 2349  
QY 781 A1aCyAaTh1eH1aAaG1yAaLeuTy1eTh1yH1aH1aH1aH1aH1aH1aH1aH1aH1a 800  
DB 2350 GCGTGCACGATTCAGGGGTCTCTACACCAACACACACACACACACACAGTATTTATCAC 2409  
QY 801 MeAa1aTh1eP1eP1eP1eP1eAaAaG1eAaG1eAaG1eAaG1eAaG1eAaG1eAaG1eAa 820  
DB 2410 ATGATCAACATTTCTTGTGAGCCCGAGATATCCGATCTATGAATGAACGATCTTACC 2469  
QY 821 SerTy11eSerValAa 840

DB 2470 TCTCAATTTCTGTGCGCATGCGCTCAGAGGTACTACGTGATGGCACTGGACCGTG 2529  
QY 841 AaP1eP1oG1yAaG1yTy1eP1eSerG1yTh1eTh1ePhaAaP1yAaAaSerTy1eAa 860  
DB 2530 GACTGGCCCGCGCGGATCAAAATTTTGAGCACTTGTGACTTACAGAGGCTCTAATAT 2589  
QY 861 G1uProG1uAaAa1e1a1eA1aTh1eG1yP1oTh1eAaAa1yTh1e1eA1aG1uAaLeu 880  
DB 2590 GAGCCGAGAACTTAATGCTTATGCTGACCAACCAAGAAACATGATTTGTGAGCTGCTG 2649  
QY 881 PheG1nG1yAaAaAaP1eP1oG1yAa1a1aTPG1uTy1eSerMeP1oAaG1e1yTh1eG1u 900  
DB 2650 TTTCAAGGAAAGAAACCGGGGTGTGCTGCTGGAATCTCATGCTCTGTTGGGAGCCGAG 2709  
QY 901 1yAaG1nProAa1aG1nProSerTy1eTh1eTPA1a1eA1aAaSerG1uCySeSerAa1 920  
DB 2710 AAGCAAGCCCTGCGCCAGCCAGCTACCTTGGCCATGATGTGGCTTCAAGTCTCGTG 2769  
QY 921 SerCyG1yG1yAaG1yAaG1yAaG1yAaG1yAaG1yAaG1yAaG1yAaG1yAaG1yAa 940  
DB 2770 TCTTGGAGAGGGGTATGATGCTTCCAGTGTGCTCTGAGGCAAGCATGTACGCTTCA 2829  
QY 941 A1aTh1a1aTy1eA1aAa 952  
DB 2830 GCCACTGCGTACATTCACCTGCTTTCTTGAATCC 2865  
RESULT 2  
US-09-981-151A-1  
Sequence 1, Application US/09981151A  
Publication No. US20030212256A1  
GENERAL INFORMATION:  
APPLICANT: Edinger, Shlomo R  
APPLICANT: Gerlach, Valerie  
APPLICANT: MacDougall, John R  
APPLICANT: Malyankar, Murtel M  
APPLICANT: Smithson, Glenda  
APPLICANT: Miller, Isabelle  
APPLICANT: Peyman, John A  
APPLICANT: Stone, David J  
APPLICANT: Gunther, Erik  
APPLICANT: Ellerman, Karen  
APPLICANT: Shimkets, Richard A  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Guo, Xiaojia  
APPLICANT: Batturajan, Meera  
APPLICANT: Taupier Jr, Raymond J  
APPLICANT: Burgess, Catherine E  
APPLICANT: Zerhusen, Bryan D  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Spytek, Kimberly A  
APPLICANT: Gangolli, Eshe A  
APPLICANT: Fernandes, Elma R  
APPLICANT: Gorman, Linda  
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-168  
CURRENT APPLICATION NUMBER: US/09/981,151A  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 60/241,040  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,058  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,063  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,243  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/242,152  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/242,482  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,611  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,612

/ PRIOR FILING DATE: 2000-10-23  
/ PRIOR APPLICATION NUMBER: 60/242,880  
/ PRIOR FILING DATE: 2000-10-24  
/ PRIOR APPLICATION NUMBER: 60/242,881  
/ PRIOR FILING DATE: 2000-10-24  
/ Remaining Prior Application data removed - See File Wrapper or PALM.  
/ NUMBER OF SEQ ID NOS: 160  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 1  
/ LENGTH: 2997  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: misc\_feature  
/ LOCATION: (857)..(858)  
/ OTHER INFORMATION: wherein n is an a or t or c or g.  
/ FEATURE:  
/ NAME/KEY: misc\_feature  
/ LOCATION: (2383)  
/ OTHER INFORMATION: wherein n is an a or t or c or g.  
/ FEATURE:  
/ NAME/KEY: misc\_feature  
/ LOCATION: (2983)  
/ OTHER INFORMATION: wherein n is an a or t or c or g.  
US-09-981-151A-1  
  
Alignment Scores:  
Pred. No.: 0 Length: 2997  
Score: 5110.00 Matches: 940  
Percent Similarity: 94.67% Conservative: 1  
Best Local Similarity: 94.57% Mismatches: 3  
Query Match: 97.59% Indels: 50  
DB: 10 Gaps: 4  
  
US-09-981-151D-8 (1-952) x US-09-981-151A-1 (1-2997)  
  
QY 1 MetLysProArgAlaArgGlyTPArgGlyLeuAlaLeuThrMetLeuLeuAlaGln 20  
DB 10 ATGAACCCCGCGCGCGGATGCGGCGCTTGCGCGCTGTGATGCTGTGGCGCAG 69  
QY 21 ValAlaGluGlnValSerProGlyArgSerHisGlnArgGlyYasnArgGlySerGlyGln 40  
DB 70 GTGGCGGAGAGAGGTGATGCCGGCGCTCCCAACACCGCGGAAACCGCGGTCCGGAACG 129  
QY 41 LeuGluAlaSerProProArgLeuLeuSerArgGlyProArgArgLeuThrAlaMetSer 60  
DB 130 CTGGAGCGAGTCCCGCGCGCTCTCTCCCGCGAACCCGCGTCTCACCGCGATGTG 189  
QY 61 ProLeuPheSerAlaGlyThrCysValArgHisGlyThrArgSerGlySerAlaTPrGlu 80  
DB 190 CCGCTGTCTTCCGACGACCTGCGGCAATGGGACCGGACCGCGCTGGATGGAAAGGCGCG 249  
QY 81 ProGluArgProAlaSerSerSerThrArgGlyAlaAlaGlyLeuAspGlyLysGlyArg 100  
DB 250 CCGGACGTCGCCGCGCTCTCTCCACCGCGGAGCGCGCGGTGGATGGAAAGGCGCG 309  
QY 101 AspMetAspGluAlaGlyYasnHisArgSerGlnGlnThrAsnThrGlyThrGluAsnGln 120  
DB 310 GACATGATGAACCTGGAACCATCGTCTCCAGCAAACTAACACAGAAACAGAAACCAA 369  
QY 121 ThrLeuHisValLeuThrGlnTyArgPheLeuValSerAlaTyArgIuValAspHisArgGly 140  
DB 370 AACATGCAATGTTCTCATCATATGACCTGGTCTTGCTTCCATGAGGTGACACAGAGGCG 429  
QY 141 AspTyArgValSerHisGluIleMetHisHisGlnArgArgArgAlaValAlaValSer 160  
DB 430 GATTACGTGTCCCATGAATCATGACCATCAGCGCGGAGGAAGACATGGCGCTGTGC 489  
QY 161 GluValGluSerLeuHisIleLeuArgLeuLysGlyProArgHisAspPheHisMetAspLeu 180  
DB 490 GAGGTGAGTCTCTTCACCTTCGGCTGAAGGCGCCACAGGACGACCTTCACATGATCTG 549  
QY 181 ArgThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlySerThrGly 200

DB 550 AGACACTTCAGAGCGCTAGTGGCTCTCGCTTATTGTGCACACGTTGGAAAGACAGCG 609  
QY 201 ThrLysSerValGlnThrLeuProProGluAspPheCysPheTyGlnGlySerLeuArg 220  
DB 610 ACTAATGCTGTGCACACTTACCGCCAGAGACTTCTGTTTCTATCAAGGCTCTTGGCA 669  
QY 221 SerHisArgAsnSerProSerHisGlyGlyLysPheCysGlyGlySerThrArgThrLeu 240  
DB 670 TCACACAGAACTCCGCATCCGATGAGGAGGAGTCTGTGAGGGCTCCACTCGCACTCG 729  
QY 241 LysLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaAlaGlnCys 260  
DB 730 AAGCTCTGACACAGTCAGAAATGTCCTCCGAGCAAGTGTGACTTCCTGCTCTCAGTGT 789  
QY 261 AlaGluHisAsnSerArgArgPheArgGlyArgHisGlyLysTyTrpLysProTyThrGln 280  
DB 790 GCGGAGCACACAGACAGACGATTCAGAGGCGGCACTACACATGGAAGCTTACACTCA 849  
QY 281 ValGluAlaAspLeuCysLysLeuTyCysIleAlaGluGlyPheAspPhePheSer 300  
DB 850 GTAGAAAGNNGACTTATGCAAACTACTGTATCGCAGAAAGATTGATTTCTTTCT 909  
QY 301 LeuSerAsnLysValLysAspGlyThrProCysSerGluAspSerArgAsnValCysIle 320  
DB 910 TTGTCAATTAAGTCAAAAGATGGAGCTCCATGCTGGAGATAGCCGTATATGTTGTATA 969  
QY 321 AspGlyIleCysGlyLeuSerValAlaSerThrSerAlaHisMetProGlnProProLys 340  
DB 970 GATGGGATATGTGACTCAGTGTGTGTCACATCTGGGCAATGCCACAGCTCCCAAG 1029  
QY 341 GluAspLeuPheIleLeuProAspGlyLysTyLysSerCysLeuArgHisLysArgSerLeu 360  
DB 1030 GAAGACCTTTCATCTTGCAGATGATGATTAAGTCTTCCATCGGCATTAAGCGCTCTCT 1089  
QY 361 LeuArgSerHisArgAsnGluGluLeuAsnValGluThrLeuValValAspLysLys 380  
DB 1090 CTGAGGCTCCATGAAGATGAAGACTGAACGTGGAGACCTGTGTGTGTCACAAAG 1149  
QY 381 MetMetGlnAsnHisGlyHisGlyAsnIleThrThrTyValLeuThrIleLeuAsnMet 400  
DB 1150 ATGATGCAAAACATAGGCACTGAATAATCAACACTACGTCTCACATCTCAACATG 1209  
QY 401 ValSerAlaLeuPheLysAsp----- 407  
DB 1210 GTATCTGCTTATATCAAAAGATGAACAATAGAGGAAACATCAACATTGCAATTGAGGT 1269  
QY 407 ----- 407  
DB 1270 CTGATTTCTTAGAAGATGAACGCCAGACTGTGATAGTCAACGACGACACACC 1329  
QY 408 -----GlyLeuMetGlyLysAspGlyThrArgHisAsp 418  
DB 1330 TTAAGTAGCTTCCGACATGGGAGTCTGATTTGATGGGAAAGATGGGACTGTGATGAC 1389  
QY 419 HisAlaIleLeuLeuThrGlyLeuAspIleCysSerTrpLysAsnGluProCysAspThr 438  
DB 1390 CACGCACTTATCTGACCTGCTGTGATATATGTTCTCGAAGAAAGAACCCCTGTGACACT 1449  
QY 439 LeuGlyPheAlaProIleSerGlyMetCysSerLysTyArgArgSerCysThrIleAsnGlu 458  
DB 1450 TTGGGATTTGCACCCATAGTGGAATGTGTAGTAATATCCGACGCTGCACGATTAATGAA 1509  
QY 459 AspThrGlyLeuGlyLeuAlaPheThrIleAlaHisGlySerGlyHisAsnPheGlyMet 478  
DB 1510 GATACAGGCTTTGAGCTGGCTTCATCATTCGCCATGAGTGTGAGCACAACATTTGGCAGT 1569  
QY 479 IleHisAspGlyGluGlyAsnMetCysLysLysSerGluGlyAsnIleMetSerProThr 498  
DB 1570 ATTCAATGATGGAGGAAGGACATGTGTAAAAAGTCCGAGGCAACATCATGTCCTTACA 1629  
QY 499 LeuAlaGlyArgAsnGlyValPheSerTrpSerProCysSerArgGlnTyLeuHisLys 518



Db 1630 TTGGCAGACGCAATGAGTCTTCTCCTGGTCACTCGACCGCCAGATATCTACCAAA 1689  
Qy PheLeuSerThrAlaGlnAlaIleCysLeuAlaAspGlnProLysProValLysGluTyr 538  
Db 1690 TTTCTAAGCACCCTCAAGTATCTGCTTGTGATCAGCCAAAGCTGTGAAGAAATAC 1749  
Qy LysTyrProGluLysLeuProGluLysTyrAspAlaAsnThrGlnCysLysTyrGln 558  
Db 1750 AAGTATCTCAGAAATTTGCGAGGAATATATGATGCAAAACACAGTCAAGTGGCAG 1809  
Qy PheGluGluLysAlaLysLeuCysMetLeuAspPheLysLysAspIleCysLysAlaLeu 578  
Db 1810 TTGGAGAGAAACCAAGCTCTGATGCTGACTTTAAAAAGACATCTGTAAAGCCCTG 1869  
Qy TrpCysHisArgIleGlyArgLysCysGluThrLysPheMetProAlaAlaGluGlyThr 598  
Db 1870 TGGTGCATCTGATTTGGAGGAATGTGAACATAATTTATGCGACGACGAAAGGCACA 1929  
Qy 11eCysGluYHisAspMetTrpCysArgGlyGlyGlnCysValLysTyrGlyAspGluGly 618  
Db 1930 ATTTGTGGGATGATGATGTGTGCGGGAGAGACAGTGTGAATATGTGTGATGAAGGC 1989  
Qy ProLysProThrHisArgLysIleTyrSerAspTrpSerSerTrpSerProCysSerArgThr 638  
Db 1990 CCCAAGCCCAACCCATGCGCACCTGCTGCGACTGCTTCTTGTCCTCCATGCTCCAGAGCC 2049  
Qy CysGlyGlyGlyValSerHisArgSerArgLeuCysThrAspProLysProSerHisGly 658  
Db 2050 TGGCGAGGGGAGATATCTCATAGAGATCGCTTGCACCAACCCCAATCCATGTCATGGA 2109  
Qy GlyLysPheCysGluGlySerThrArgThrLeuLysLeuCysAsnSerGlnLysCysPro 678  
Db 2110 GGGAGATTTCTGTAGGGGCTCACTCGCACTGTGAAGCTTGCAACAGTCAAGATATGCC 2169  
Qy ArgAspSerValAspPheArgAlaAlaGlnCysAlaGluHisAsnSerArgAspPheArg 698  
Db 2170 CGGAGAGAGTGTATCTCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2229  
Qy GlyArgHisTyrLysTyrLysProTyrThrGlnValGluAspGlnAspLeuCysLysLeu 718  
Db 2230 GGGCGGCACTACAAAGTGAAGCCT-----CAGGACTTATGCAAACTC 2271  
Qy TyrCysIleAlaGluGlyPheAspPhePhePheSerLeuSerAsnLysValLysAspGly 738  
Db 2272 TACTGATCGCAGAGATTTGATTTCTTTCTTTTCTTTGCAATTAAGTCAAAAGATGGG 2331  
Qy ThrProCysSerGluAspSerArgAsnValCysIleAspGlyLleCysGluAspValGly 758  
Db 2332 ACTCCATGCTCGAGAGATACCCGTAATGTTGTATGATGGAGATATGTGAG--NTTGA 2388  
Qy CysAspAsnValLeuGlySerAspAlaValGluAspValCysGlyValCysAsnGlyAsn 778  
Db 2389 TGTGACAAATGTTCTTGATGTGATGCTGTGTAAGACCTGTGGGGGTGTAAACGGGAAT 2448  
Qy AsnSerAlaCysThrIleHisArgGlyLeuTyrThrLysHisHisHisIleThrAsnGlnTyr 798  
Db 2449 AACTCAGCGCGCAGATTCACAGGGGTCTTACACCAAGACACACACCAACAC---CAT 2505  
Qy TyrHisMetValThrIleProSerGlyAlaArgSerIleArgIleTyrGluMetAsnVal 818  
Db 2506 TATCACAATGTGTACCAATCTTCTGTGAGCCCGAGATATCCGACATATGAAGAAACGCTC 2565  
Qy SerThrSerTyrIleSerValArgAsnAlaLeuArgArgTyrTyrLeuAsnGlnLysIleTyr 838  
Db 2566 TCTAATCTCTCAATTTCTGTGCGCAATGCCCTCAGAAAGTACTAATCTGAATGGGCACTGG 2625  
Qy ThrValAspTrpProGlyArgTyrLysPheSerGlyThrThrPheAspTyrArgArgSer 858  
Db 2626 ACCGTGAGTGGCGCGCGCGGTCAAAATTTTCGGGCGACTCTTTCGACTACAGACGGTCC 2685  
Qy TyrAsnGluProGluAsnLeuIleAlaThrGlyProThrAsnGluThrLeuIleValGlu 878  
Db 2686 TATTAATGAGCCCGAGAACTTAATCGCTATGAGCAACCAAGAGACACTGATTTGTGGAG 2745

Qy 879 LeuLeuPheGlnGlyArgAsnProGlyValAlaTyrGluTyrSerMetProArgLeuGly 898  
Db 2746 CTGCTCTTCAAGGAGAAAGAACCGGGGTGTGCTGTGGAAATGCTCATGCTGCTGGGG 2805  
Qy 899 ThrGluLysGlnProProAlaGlnProSerTyrThrTyrAlaIleValArgSerGluCys 918  
Db 2806 ACCGAGAACAGCCCTCCCTCCAGCCAGCTACACTTGGGCCATCTGTGCTCTGAGTGC 2865  
Qy 919 SerValSerCysGlyGlyGlyArgCysLeuProValLeuLeuGlnAlaAlaCysGln 938  
Db 2866 TCCGTGTCTCGGAGAGGGGTAGTCTCTTCAAGTCTGCTCTGAGGAGCAGATCTCAG 2925  
Qy 939 ProSerAlaThrAlaTyrIleAlaLeuAlaPheLeuGluSer 952  
Db 2926 CTTTCAAGCCACTGCGTACATTTGCACTTGCGCTTTCTTGAATCC 2967  
  
RESULT 3  
US-09-981-151A-3  
Sequence 3, Application US/09981151A  
Publication No. US20030212256A1  
GENERAL INFORMATION:  
APPLICANT: Edinger, Shlomit R  
APPLICANT: Gerlach, Valerie  
APPLICANT: MacDougall, John R  
APPLICANT: Malyankar, Muriel M  
APPLICANT: Smithson, Glenda  
APPLICANT: Millet, Isabelle  
APPLICANT: Beyman, John A  
APPLICANT: Stone, David J  
APPLICANT: Gunther, Erik  
APPLICANT: Ellerman, Karen  
APPLICANT: Shimkets, Richard A  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Guo, Xisaojia  
APPLICANT: Paturajan, Meera  
APPLICANT: Taupier Jr, Raymond J  
APPLICANT: Burgess, Catherine E  
APPLICANT: Zerhusen, Bryan D  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Spytek, Kimberly A  
APPLICANT: Gangolli, Saba A  
APPLICANT: Fernandes, Elma R  
APPLICANT: Gorman, Linda  
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-168  
CURRENT APPLICATION NUMBER: US/09/981,151A  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 60/241,040  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,058  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,063  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,243  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/242,152  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/242,482  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,611  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,612  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,880  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/242,881  
PRIOR FILING DATE: 2000-10-24  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 2433

```

: TYPE: DNA
: ORGANISM: Homo sapiens
us-09-981-151A-3

Alignment Scores:
Pred. No.: 0 Length: 2433
Score: 4103.50 Matches: 774
Percent Similarity: 82.16% Conservative: 9
Best Local Similarity: 81.22% Mismatches: 7
Query Match: 78.37% Indels: 163
DB: 10 Gaps: 8

US-09-981-151D-8 (1-952) x US-09-981-151A-3 (1-2433)

QY 1 MetLysProArgAlaArgGlyTTPArgGlyLeuAlaLeuTTPMetLeuAlaGln 20
DB 31 ATGAAGCCCGCGCGCGGATGGCGGGCTTGCGCGCTGTGATGTGCTGGCGGCG 90
QY 21 ValAlaGlnGlnValSerProGlyArgSerHisGlnArgGlyAsnArgGlySerGlyGln 40
DB 91 GTGGCCGAGCAGGTGAGTCCCGGGCGCTCCACACGCGGGAACCGCGGTCGCGACG 150
QY 41 LeuGluAlaSerProProArgLeuLeuSerArgGlyProArgArgLeuThrAlaMetSer 60
DB 151 CTGGAGGCGAGTCCCGCGGCTCTCTCCGCGGACCCGCGCTTCACCGCGATGTCG 210
QY 61 ProLeuPheSerAlaGlyThrCysValArgHisGlyThrArgSerGlySerAlaTTPGlu 80
DB 211 CGGCTGTTTCCGACGAGCACCTGCGTGGCGCATGGGACCGCGAGCGCGCTTGAGG 270
QY 81 ProGluArgProAlaSerSerSerThrArgGlyAlaAlaGlyLeuAspGlyLysGlyArg 100
DB 271 CCCGAGCGTCCCGCGCTCTCTCCACCCGCGAGCGCGCGCTGGATGAAAGGCGG 330
QY 101 AspMetAspGlyAlaGlyAsnHisArgSerGlnGlnThrAsnThrGlyThrGluAsnGln 120
DB 331 GACATGATGAAAGCTGGAAACCATCTTCTCACGAAACTTAACACAGGAACAGAAACCA 390
QY 121 ThrLeuHisValLeuThr---GlnTyraAspLeuValSerAlaTyrGluValAspHisArg 139
DB 391 AACAGTCATGTTCTCTCACTCGTGAATATGACCTGGTCTTGCTTACGAGGTTGACCA 450
QY 140 GlyaAspTyrValSerHisGlnLysLeuMetHisHisGlnArgArgArgAlaValAlaVal 159
DB 451 GCGGATTAAGTGTCCCATGAATATCATGACCATGACGCGGAGGAAGACAGTGGCCGG 510
QY 160 SerGluValAlaGlySerLeuHisLeuArgLeuLysGlyProArgHisAspPheHisMetAsp 179
DB 511 TCGAGAGTTGAGTCTTCACTTCCTCGCTGMAAGGCCCAAGGACGACATTCACATGAT 570
QY 180 LeuArgThrSerSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThr 199
DB 571 CTGAGGACTTCCAGCGAGCTAGTGGCTCTGGCTTTATGTGCAGACGTGGGAAAGACA 630
QY 200 GlyThrLysSerValGlnThrLeuProProGluAspPheCysPheTyrGlnGlySerLeu 219
DB 631 GGCACTAACTCTGTGAGACTTTACCCGCAAGAGACTTCTGTTTCTATAAAGCTCTTGG 690
QY 220 ArgSerHisArgAsnSerProSerHisGlyLysLysPheCysGlyGlnGlySerThrArgThr 239
DB 691 CGATCAACAGAAATCTCCCATCGCATGGAGGAAGTCTGTGAGGGCTCCACTCGCACT 750
QY 240 LeuLysLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaAlaGln 259
DB 751 CTGAAGCTCTGCAACAGTCAAAATGTCCCGGAGACAGTGTGACTTCCGCTCTGCTCAG 810
QY 260 CysAlaGlnHisAsnSerArgArgPheArgGlyArgHisIleTyrLysThrLysProTyrThr 279
DB 811 TGTGCGAGCAACAACGACAGCATTCAGAGGCGGCACTACAAAGTGAAGGCTTAACT 870
QY 280 GlnValGluAlaAspLeuCysLysLeuTyrCysIleAlaGlnGlyPheAspPhePhe 299
DB 871 CAAGTAAAGAACAGACTTATGAAACTCTACTGTATGCGAAGAGATTGATTTCTTTCTTT 930
```

```

QY 300 SerLeuSerAsnLysValLysAspGlyThrProCysSerGluAspSerArgAsnValCys 319
DB 931 TCTTTGTCAATTAAGTCAAGATGGAATGCACTCATCTCGAGAGATAGCGTATGTTTGT 990
QY 320 IleAspGlyIleCysGlnLeuSerValValSerThrSerAlaHisMetProGlnProPro 339
DB 991 ATAGATGGGATATGGAG-----ATGCCGAGGCTCTCC 1023
QY 340 LysGluAspLeuPheIleLeuProAspGlyTyrTyrLysSerCysLeuArgHisLysArgSer 359
DB 1024 AAGGAAGCTCTTATATCTTGCAGATGAGTATAGTCTTGCTTACGGCATAAAGGCTCT 1083
QY 360 LeuLeuArgSerHisArgAsnGlnGluLeuAsnValGluThrLeuValValLysLys 379
DB 1084 CTTCGAGGTCCCATAGAATGAAGAACTGAACGCGAGACCTTGCTGTGTCAGACAA 1143
QY 380 LysMetMetGlnAsnHisGlyHisGlnAsnIleThrTyrTyrValLeuThrIleLeuAsn 399
DB 1144 AAGATGATGCAAAACCATAGGCGCATGAAATATACACACCTACGTGCTACGATACTCAAC 1203
QY 400 MetValSerAlaLeuPheLysAspGlyLeuMetGlyLysAspGlyThrArgHisAspHis 419
DB 1204 ATGATATCTGCTTATATTCAAAGATGGAACATAGCA----- 1239
QY 420 AlaIleLeuLeuThrGlyLeuAspIleCysSerTTPLysAsnGluProCysAspThrLeu 439
DB 1239 ----- 1239
QY 440 GlyPheAlaProIleSerGlyMetCysSerLysTyrArgSerCysThrIleAsnGluAsp 459
DB 1239 ----- 1239
QY 460 ThrGlyLeuGlyLeuAlaPheThrIleAlaHisGlnSerGlyHisAsnPheGlyMetIle 479
DB 1239 ----- 1239
QY 480 HisAspGlyGlnGlyAsnMetCysLysLysSerGlnGlyAsnIleMetSerProThrLeu 499
DB 1240 -----GAAACATC--AACATTGCAATT 1260
QY 500 AlaGlyArgAsnGlyValPheSerTTPSerProCysSerArgGlnTyrLeuHisLysPhe 519
DB 1261 GTAGGT----- 1266
QY 520 LeuSerThrAlaGlnAlaIleCysLeuAlaAspGlnProLysProValLysGlyLys 539
DB 1266 ----- 1266
QY 540 TyrProGluLysLeuProGlyGluLeuTyrAspAlaAsnThrGlnCysLysTTPGlnPhe 559
DB 1266 ----- 1266
QY 560 GlyLysLysAlaLysLeuCysMetLeuAspPheLysLysAspIleCysValAlaLeuTTP 579
DB 1267 -----CTAATTTCTTGAAGATGAGTACAGACATCTGTAAAGCCCTGTAG 1311
QY 580 CysHisArgIleGlyArgLysCysGlyIleThrLysPheMetProAlaAlaGlnGlyThrIle 599
DB 1312 TGCCATGCTATTTGAAGGAATGTGAGACTTAATTATGCCAGACGAGAGGCAATTT 1371
QY 600 CysGlyHisAspMetTTPCysArgGlyGlyGlnCysValLysTyrGlyLysAspGlyLysPro 619
DB 1372 TGTGGCATGACATGTGCTGCGGGGAGGACAGTGTGAAATATGTGATGAAGAGGCCCC 1431
QY 620 LysProThrHisGlyHisIleTTPSerAspTTPSerSerTTPSerProCysSerArgThrCys 639
DB 1432 AAGCCACCAATGGCACTGGTGGACTGTGCTTGTGGTCCCATGCTCCAGACCTGTC 1491
QY 640 GlyGlyGlyValSerHisArgSerArgLeuCysThrAsnProLysProSerHisGlyGly 659
DB 1492 GAGAGGGAGTATCTCATAGGAGTGCCTCTGCAACCAACCCAGGCAATGCCATGGAAGG 1551
```

QY 660 LysPheCysGluGlySerThrArgThrLeuLysLeuCysAsnSerGlnLysCysProArg 679  
DB 1552 AAGTTCTGTAGGGGCTTCACTCGCATCTGAAGCTTGCAGAACGTGCAAGAAATGCCCCGG 1611  
QY 680 AppSerValAspPheArgAlaAlaGlnCysAlaGlnHisAsnSerArgPheArgGly 699  
DB 1612 GACAGGTGTGACTTCCGTGCTCAAGTGTGCGAGACAAACGACATTCAGAGGG 1671  
QY 700 ArgHisTyrLysTyrLysProTyrThrGlnValGluAspGlnAspLeuCysLysLeuTyr 719  
DB 1672 CGGCACCTACAAAGTGAAGCT-----CAGACCTTATCAAACTCTAC 1713  
QY 720 CysIleAlaGlnGlyPheAspPhePhePheSerLeuSerAsnLysValLysAspGlyThr 739  
DB 1714 TGATCGCAGAGAGATTGATTCTTCTTCTTCTTGTCAATTAAGTCAAAGATGGGACT 1773  
QY 740 ProCysSerGluAspSerArgAsnValCysIleAspGlyLecysGlyLysValGlyCys 759  
DB 1774 CCATGCTCGGAGAGATAGCCCTTAATGTTGTATGATGGGATATGTAG-----GGATGT 1827  
QY 760 AppAsnValLeuGlySerAspAlaValGluAspValCysGlyValCysAsnGlyAsnAsn 779  
DB 1828 GACAAAGTCTTGTGACTGTAGTCTTTGAAGACGCTGTGGGGTGTATACGGGAATAC 1887  
QY 780 SerAlaCysThrIleHisArgGlyLeuTyrThrLysHisHisHisThrAsnGlnTyrTyr 799  
DB 1888 TCAGCCTGCACGATTCACAGGGGCTCTTACACCAAGACCAACCAACCAAC---TATTAT 1944  
QY 800 HisMetValThrIleProSerGlyAlaArgSerIleArgIleTyrGluMetAsnValSer 819  
DB 1945 CACATGCTCACATTCCTTCTTGAGACCGCGAGATACCGCATCTATGAAATGAACGCTCT 2004  
QY 820 ThrSerTyrIleSerValArgAsnAlaLeuArgArgTyrTyrLeuAsnGlnHisTyrThr 839  
DB 2005 ACCTCTCACTTCTGTGCGCAATGCCCTGAGAAAGTACTGATGGGCACTGGACC 2064  
QY 840 ValAspTyrProGlyArgTyrLysPheSerGlyThrThrPheAspTyrArgArgSerTyr 859  
DB 2065 GTGGACGTGGCGCGCGGTGCAAAATTTTGGGCACTACTTTCAGACTACAGACGCTCTAT 2124  
QY 860 AsnGluProGluAsnLeuIleAlaThrGlyProThrAsnGluThrLeuIleValGluLeu 879  
DB 2125 AAGAGACCCCAAGAACTTAATCGCTACGAGCAACCAACGACGATGTGGAGCTG 2184  
QY 880 LeuPheGlnGlyArgAsnProGlyValAlaIleArgGluTyrSerMetProArgLeuGlyThr 899  
DB 2185 CTGTTCAGGGAAGAAACCCGGGGTGTGCTGTGGAAATCTCAATGCCCTCTTGGGGACC 2244  
QY 900 GluLysGlnProProAlaGlnProSerTyrThrTyrAlaIleValArgSerGlnCysSer 919  
DB 2245 GAGAACAGACCCCTCGCCACGCCCAAGTCACTTGGGCCATCGTGGCTCTGAGTCTCC 2304  
QY 920 ValSerCysGlyGlyGlyArgCysLeuProValLeuLeuGluAlaAlaCysGlnPro 939  
DB 2305 GTGTCTCGCGAGGGGTAGTGTCTTCCAGTGTCTGTCTGTGAGGACAGCATGTACAGCT 2364  
QY 940 SerAlaThrAlaTyrIleAlaLeuAlaPheLeuGluSer 952  
DB 2365 TCAGCCACTGCGTACATGCACTGGCTTCTTGAATCC 2403

RESULT 4  
US-10-330-176-1  
/ Sequence 1, Application US/10330176  
/ Publication No: US20030228676A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Agostino, Michael  
/ APPLICANT: DiBlasio, Elizabeth  
/ TITLE OF INVENTION: AGGRECANASE MOLECULES  
/ FILE REFERENCE: AM100884  
/ CURRENT APPLICATION NUMBER: US/10/330,176  
/ CURRENT FILING DATE: 2002-12-30  
/ PRIOR APPLICATION NUMBER: 60/344,895  
/ PRIOR FILING DATE: 2001-12-31

/ NUMBER OF SEQ ID NOS: 18  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 1  
/ LENGTH: 3675  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
US-10-330-176-1

Alignment Scores:  
Pred. No.: 0  
Score: 3993.50  
Percent Similarity: 78.36%  
Best Local Similarity: 76.75%  
Query Match: 76.27%  
DB: 17  
Length: 3675  
Matches: 766  
Conservative: 16  
Mismatch: 37  
Indels: 181  
Gaps: 10

US-09-981-151d-8 (1-952) x US-10-330-176-1 (1-3675)

QY 1 MetLysProArgAlaArgGlyTyrArgGlyLeuAlaAlaLeuTyrMetLeuLeuAlaGln 20  
DB 1 ATGAAAGCCCGCGCGCGGATGGCGGGCTTGGCGCGCTGTGATGCTGTGGCGCAG 60  
QY 21 ValAlaGluGlnValSerProGlyArgSerHisGlnArgGlyAsnArgGlySerGlyGln 40  
DB 61 GTGGCCGAGCA----- 71  
QY 41 LeuGluAlaSerProArgLeuLeuSerArgGlyProArgArgLeuThrAlaMetSer 60  
DB 71 ----- 71  
QY 61 ProLeuPheSerAlaGlyThrCysValArgHisGlyThrArgSerGlySerAlaTyrGlu 80  
DB 72 -----GGACCTGTGCTGCGCCCATGGGACCGCGAGCGCGGCTGGAG 116  
QY 81 ProGluArgProAlaSerSerSerThrArgGlyAlaAlaGlyLeuAspGlyLysGlyArg 100  
DB 117 CCCGAGCGTCCCGCGCTCTCCACCCCGAGCGCGCGGTGATGAAAGGCG-- 174  
QY 100 GAspMetArgGluAlaGlyAsnHisArgSerGlnGlnThrAsnThrGlyThrGluAsnGln 120  
DB 174 ----- 174  
QY 120 nThrLeuHisValLeuThrGlnTyrAspLeuValSerAlaTyrGluValAspHisArgGln 140  
DB 175 -----GAATATACCTGTGCTGTGCTGCTGCTGAGAGTTGACACAGCGGG 215  
QY 140 yAspTyrValSerHisGlnIleMetHisHisGlnArgArgArgAlaValAlaValSer 160  
DB 216 CGATTACGTGTCCCATGAAATCATGACACATGACGCGCGAGAAAGCAGTGGCGTGT 275  
QY 160 rGluValGluSerLeuHisLeuArgLeuLysGlyProArgHisAspPheHisMetAspLe 180  
DB 276 CGAGGTGAGTCTCTTCACTTGGCTGAAAGGCCCAAGGACGACATTCACATGGATCT 335  
QY 180 yArgThrSerSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrGln 200  
DB 336 GAGGACTTCCAGAGAGCTGATGGCTCTGCTTATTTGTCAGAGACTTGGGAAAGCAG 395  
QY 200 yThrLysSerValGlnThrLeuProProGluAspPheCysPheTyrGlnGlySerLeuArg 220  
DB 396 CACTAAGTCTGTGACAGACTTTCACCGCAGAGACTTCTTCTTCAAGAGGCTCTTGG 455  
QY 220 gSerHisArgAsnSerProSerHisGlyLysPheCysGlyLysSerThrArgThrLe 240  
DB 456 ATCACAACAGAACTCC--TCAGTGGCCCTTTCAACCTGCAAGGCTTGTGAGCATGAT 512  
QY 240 uLysLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaAlaGlnCys 260  
DB 513 ACAG-----ACAGAAAGGAGCATTTACTTCTTAAGGCACT 548  
QY 260 sAlaGlnHisAsnSerArgArgPheArgGlyArgHisTyrLysTyrLysProTyrThrGln 280  
DB 549 TCCTTCACACCTCTCA-----TGAAA----- 570

QY 280 nValGluAlaAspLeuCybLysLeuTyrCybIle-AlaGluGlyPheAspPhePhePheS 300  
Db 571 -----CTCGGACAGAG----- 580  
QY 300 exLeuSerAenLysValLysAspGlyThrProCysSerGlyAspSerArgAenValCysI 320  
Db 581 --CTGCCCAAGGACGCTGCCATCCACGATCTGTACAGAGATCCACAGAGGCCCATCG 638  
QY 320 LeuAspGlyIleCybGlyLeuSerValLysSerThrSer-----AlaHis----- 334  
Db 639 TCCT-GGGGGCAGTGAAGTCTGTGTGACCTCAAGGACATGGGAGCTGGACATCAACCCC 697  
QY 334 ----- 334  
Db 698 TGCACAGACGCACTTCGCTGGAGCTGCCACAAAAGCAGATTCTGTGAAGAAGCGCA 757  
QY 335 -----MetProGlnProProLysGlyLysAspLeuPheIleLeuProAspGlyTyrLys 352  
Db 758 AGAAATACATGCCCGCCAGCTCCCAAGGAGAGCCTTTCATCTTGCAGAGATGATTAAGT 817  
QY 352 exCybLeuArgHisLysArgSerLeuLeuArgSerHisArgAenGlyLysLeuAenValG 372  
Db 818 CTGGCTTAAGGCAATAAGCGCTCTTCTGAGGTCCCATGAATGAAGAATGAAGTGAAGTGG 877  
QY 372 LuThrLeuValValValAspLysLysMetMetGlnAenHisGlyHisGlyAenIleThrT 392  
Db 878 AGACCTTGTTGGTGTGTCGACAAAGATGATGCAAAACCATGCGCATGAAATATCACCAC 937  
QY 392 hTyrValLeuThrIleLeuAenMetValSerAlaLeuPheLysAsp----- 407  
Db 938 CCAAGCTGCTCAGATACATCAATGTGATCTGCTTATTCAAAAGATGAACATATGAGAG 997  
QY 407 ----- 407  
Db 998 GAACAATCAACATTGCATTGTAGTCTGATTTCTTGAAGATGAACGCCAGAGACTGG 1057  
QY 408 -----GlyLeuM 410  
Db 1058 TGATAAGTACACAGCAGACACACCTTAAGTAGCTTGCAGTGGCAGTCTGAGTTGA 1117  
QY 410 exGlyLysAspGlyThrArgHisAspHisAlaIleLeuLeuThrGlyLysAspIleCysS 430  
Db 1118 TGGGGAAGAAATGGGACTCGTCATGACACAGCCCATTTACTGACTGTCTGGATATATGTT 1177  
QY 430 exTyrLysAenGlyProCysAspThrLeuGlyPheAlaProIleSerGlyMetCysSerL 450  
Db 1178 CCTGGAAGATGAGCCCTGTGACATTTGGGATTTGCACCCATTAAGTGAAGTGTGAAGTA 1237  
QY 450 yATyrArgSerCysThrIleAenGlyAspThrGlyLeuGlyLeuAlaPheThrIleAlaH 470  
Db 1238 AATATGCGAGCTGCAGATTAAGAAATACAGTCTTGAGCTGGCCTTTCACCATTTGCC 1297  
QY 470 LeuLysSerGlyHisAenPheGlyMetIleHisAspGlyGlyLysAenMetCysLysLys 490  
Db 1298 ATGAGCTTGACACAACTTTGGCATATTCATGATGAGAGAGGAGAACATGTAAAAAGT 1357  
QY 490 exGlyLysAenIleMetSerProThrLeuAlaGlyArgAenGlyValPheSerTyrSerP 510  
Db 1358 CCGAGGGGCAACATCATGTCCCTCATATGGCAGAGAGCATGGAGTCTTCTCTGTGTAC 1417  
QY 510 rCCysSerArgGlnTyrLeuHisLysPheLeuSerThrAlaGlnAlaIleCybLeuAla 530  
Db 1418 CCTGACGCGCGAGTACTACACAAATTTCTAAGCACCCTCAAGTATCTGCTTGGCTG 1477  
QY 530 sPGlnProLysProValLysGlyTyrLysTyrProGlyLysLeuProGlyGlyLysLeuTyrA 550  
Db 1478 ATCAGCGCAAGCCTGTGAAGAAATACAGATATCTTAAGAAATTTGCCAGAGAAATTAATG 1537  
QY 550 sPAlaAenThrGlnCybLysTyrPGLnPheGlyGlyLysAlaLysLeuCybMetLeuAspP 570  
Db 1538 ATGCAAAACACAGTGCAGTGGCAGTTCTGGAGAGAAAGCCAAAGCTCTGCATGCTGGA 1597

QY 570 hLysLysAspIleCybLysAlaLeuTyrCysHisArgIleGlyArgLysCybGlyThrL 590  
Db 1598 TTTAAAGGACATCTGTAAAGCCCTGTGTGCATGTATTTGAAGAAATGTGAGACTTA 1657  
QY 590 yAPheMetProAlaIaGlyGlyThrIleCysGlyHisAspMetTyrCysArgLysGlyG 610  
Db 1658 AATTTATGCGACAGACAGAGAGACAAATTTGTGGGCAAGCATGTGTGTCCGGAGAGAC 1717  
QY 610 InCybValLysTyrGlyAspGlyGlyProLysProThrHisGlyHisTyrSerAspTyrS 630  
Db 1718 AGTGTGAAATATATGTGTATGAAAGGCCCAAGCCCAACCATGCGCATGCTGTGACTGT 1777  
QY 630 exSerTyrSerProCysSerArgThrCybGlyGlyGlyValSerHisArgSerArgLeu 650  
Db 1778 CTTCCTTGGCCCAAGCTCCAGAGCTCGGAGGGGAGTATCTCATAGAGATCGCTCT 1837  
QY 650 yAThrAspProLysProSerHisGlyGlyLysPheCybGlyLysSerThrArgThrLeuL 670  
Db 1838 GCACCAACCCCAAGCCATCGCATGGAGGAGAGTCTGTGAGGGGCTTCCACTCCACTTGA 1897  
QY 670 yALeuCysAenSerGlnLysCysProArgAspSerValAspPheArgAlaIaGlnCysA 690  
Db 1898 AGCTCTGCAACAGTCAGAAATGTCCCGGAGCAGTGTGACTTCGCTGTGCTCAGTGTG 1957  
QY 690 IaGlyHisAenSerArgArgPheArgGlyArgHisTyrLysTyrLysProLysTyrThrGln 710  
Db 1958 CCGAGCACAAACGACAGAGATTCAGAGGGCGGCACATCAAGAGAAAGCTTACATCAAG 2017  
QY 710 aGlyAspGlnAspLeuCybLysLeuTyrCysIleAlaGlyLysPheAspPhePhePheS 730  
Db 2018 TAGAAGATCAGGACTTAATGCAACTTACTGTATGCGAAGAGATTTGATTTCTTCTTT 2077  
QY 730 exLeuSerAsnLysValLysAspGlyThrProCysSerGlyLysAspSerArgAenValCysI 750  
Db 2078 CTTCCTCAAAATTAAGTCAAAAGATGGAGCTCCATGCTCGAGAGATAGCGTAAATGTTGTA 2137  
QY 750 LeuAspGlyIleCybGlyLysArgValGlyCysAspAenValLeuGlySerSerAlaValGly 770  
Db 2138 TAGATGGAGATATGATGAGAGATGTGATGTGACAAATGCTTGGATCTGATGTGTTGAAG 2197  
QY 770 sPValCybGlyValCybAenGlyAenAenSerAlaCysThrIleHisArgGlyLeuTyrT 790  
Db 2198 AGCTGTGTGGGTGTGTAAACGGAAATATCTAGCTGCACATTTACAGGGGTCTCTACA 2257  
QY 790 hTyrHisHisHisThrAenGlnTyrTyrHisMetValThrIleProSerGlyAlaArgS 810  
Db 2258 CCAAGCACACACACACAGATATTAATCAGATGTCACCATTCCTTCTGAGCCCGGA 2317  
QY 810 exIleArgIleTyrGlyMetAenValSerThrSerTyrIleSerValArgAenAlaLeuA 830  
Db 2318 GTATCCGATCTATTAATAATGAACGTCTTACTCTTACATTTCTGTGGCAATGCCCTCA 2377  
QY 830 rGArgTyrTyrLeuAenGlyHisTyrThrValAspTyrProGlyLysTyrLysPheSerG 850  
Db 2378 GAGGTACTACTGTAATGGGACTGTGACCTGTGACTGGCCCGCGCGGTACAAATTTTGG 2437  
QY 850 LuThrThrPheAspTyrArgArgSerTyrAenGlyProGlyLysAenIleAlaThrGlyP 870  
Db 2438 GCATTAATTTGACATACAGACGGTCTTAATTAAGACCCGAGAACTTAATCGCTACTGAGC 2497  
QY 870 rOTHrAenGlyThrLeuIleValGlyLeuLeuPheGlnGlyValArgAenProGlyValAlaI 890  
Db 2498 CAACCAAGAGACATGATTGTGGAGCTGTGTTCAAGGAGAAAGAAACCCGGGTGTGTGCT 2557  
QY 890 rPGlyTyrSerMetProArgLeuGlyThrGlyLysGlnProProAlaGlnProSerTyrT 910  
Db 2558 GGGAAATCTCATGCTGCTGTGGGAGCCGAGAGAGACCCCTTCCAGCCACTTACA 2617  
QY 910 hTTPAlaIleValArgSerGlyCysSerValSerCysGlyGlyArg 926  
Db 2618 CTGGGCAATGATGCTGTGATGCTCTCGTGTCTCTGCGAGGGGGAGCAG 2667

RESULT 5

US-10-275-107-16  
; Sequence 16, Application US/10275107  
; Publication No. US20040063107A1  
; GENERAL INFORMATION:  
; APPLICANT: PLOMMAN, GREGORY D.  
; APPLICANT: WHITE, DAVID  
; APPLICANT: SUDARSANAM, SUCHA  
; APPLICANT: MANNING, GERARD  
; APPLICANT: CAENEPEEL, SEAN R.  
; APPLICANT: PAYNE, VILIA  
; TITLE OF INVENTION: NOVEL PROTEASES  
; FILE REFERENCE: 038602/1479  
; CURRENT APPLICATION NUMBER: US/10/275,107  
; CURRENT FILING DATE: 2003-11-03  
; PRIOR APPLICATION NUMBER: PCT/US01/14431  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: 60/201,879  
; PRIOR FILING DATE: 2000-05-04  
; NUMBER OF SEQ ID NOS: 105  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 3675  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-275-107-16  
  
Alignment Scores:  
Prod. No.: 0 Length: 3675  
Score: 3993.50 Matches: 766  
Percent Similarity: 78.36% Conservative: 16  
Best Local Similarity: 76.75% Mismatches: 37  
Query Match: 76.27% Indels: 181  
DB: 18 Gaps: 10  
  
US-09-981-151D-8 (1-952) x US-10-275-107-16 (1-3675)  
  
QY 1 MetLysProArgAlaArgGlyTTPArgGlyLeuAlaLeuTPMetLeuLeuAlaGln 20  
Db 1 ATGAAGCCCGCGCGCGGATGGCGGGCTTGCGCGGCTGTGATGCTGCGCGCAG 60  
QY 21 ValAlaGluGlnValSerProGlyArgSerHisGlnArgGlyAsnArgGlySerGlyGln 40  
Db 61 GTGGCCGACGA----- 71  
QY 41 LeuGluAlaSerProProArgLeuLeuSerArgGlyProArgArgLeuThrAlaMetSer 60  
Db 71 ----- 71  
QY 61 ProLeuPheSerAlaGlyThrCyValArgHisGlyThrArgSerGlySerAlaTPGlu 80  
Db 72 -----GGCACCTGTGCTGGCCATGGGACCCGCGACGGCGGCGCTGGGAG 116  
QY 81 ProGluArgProAlaSerSerSerSerThrArgGlyAlaAlaGlyLeuAspGly-LysGlyArg 100  
Db 117 CCGGAGCGCTCCGCGTCTCTCTCCACCCGCGAGCGCGCGGCTGATGAAAAAGGCGC-- 174  
QY 100 GAspMetAspGluAlaGlyAsnHisArgSerGlnGlnThrAsnThrGlyThrGluAsnGln 120  
Db 174 ----- 174  
QY 120 nThrLeuHisValLeuThrGlnTyrAspLeuValSerAlaTyrGluValAspHisArgGly 140  
Db 175 -----GAAATATGACCTGGTCTCTGCTTACGAGGTTGACCAACGAGGG 215  
QY 140 YAspTyrValSerHisGluTyrLeuMetHisGlnHisArgArgArgAlaValAlaValSe 160  
Db 216 CGATTAGGTGTCCCATTAATCATGACCAATGACGCGCGGAGAAAGACAGTGGCGGTGTC 275  
QY 160 rGluValGluSerLeuHisLeuArgLeuLeuGlyProArgHisAspPheHisMetAspLe 180  
Db 276 CGAGGTGAGTCTTCTTACCTTGCGCTGAAGGCGCCAGGAGCACTTCCACATGGATCT 335  
QY 180 uArgThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrGln 200

Db 336 GAGAGCTTCCAGACGAGCTGAGCTCTGCTTATTTGCAACCTTGGAAAGACAGG 395  
QY 200 YThrLysSerValGlnThrLeuProProGluAspPheCysPheTyrGlnGlySerLeuArg 220  
Db 396 CACTTAAGTCTGTCAACACTTTACCGCAAGGACTTGTGTTATCAAAAGGCTTTTGCG 455  
QY 220 gSerHisArgAsnSerProSerHisGlyGlyLysPheCysGluGlySerThrArgThrLe 240  
Db 456 ATCACACAGAAATCTCC---TCAGTGGCCCTTTCAACTGCAAGCTTGTCAGGCAATGAT 512  
QY 240 uLysLeuCyAsnSerGlnLysCyAspArgAspSerValAspPheArgAlaAlaGlnCy 260  
Db 513 ACGA-----ACAGAAGAGGACGATTACTTCTTAAGGCCACT 548  
QY 260 sAlaGluHisAsnSerArgArgPheArgGlyArgHisTyrLysThrLysProTyrThrGln 280  
Db 549 TCCTTCACACTTCTCA-----TGAAA----- 570  
QY 280 nValGluAlaAspLeuCyLeuLeuTyrCysIle-AlaGluGlyPheAspPhePhePheS 300  
Db 571 -----CTCGGCAAG----- 580  
QY 300 eLysSerAsnLysValLysAspGlyThrProCysSerGluAspSerArgAsnValCysI 320  
Db 581 --CTGCCAAAGCAGCTCGCCATCCACGTACTGTCAAGAGATCCACAGAGCCCATGC 638  
QY 320 LeAspGlyLysCysGluLeuSerValValSerThrSer-----AlaHis----- 334  
Db 639 TCCT--GGGGCAAGTGAAGTCTGTGTGACCTCAAGACATGGAGAGCTGGCAATCAACCCC 667  
QY 334 ----- 334  
Db 698 TGCACAGACGACGACTTCGCGCTGGACTGCCAAGAAAGCAGCATTTCTGTGAAGAGCGCA 757  
QY 335 -----MetProGlnProProLysGluAspLeuPheIleLeuProAspGlyTyrLys 352  
Db 758 AGAAATATACATGCCCCGAGCTCCCAAGAAAGACCTTCTCACTTGGCCAGATGAGTATTAAG 817  
QY 352 eCysLeuLeuArgHisLysArgSerLeuLeuArgSerHisArgAsnGlnGluLeuAsnValG 372  
Db 818 CTTCCTTACGGCATAAGCCCTCTCTTCTGAAGTCCATGAATGAAGAACTGAAGCGTGG 877  
QY 372 lThrLeuValValAlaAspLysLysMetMetGlnAsnHisGlyHisGluAsnIleThrT 392  
Db 878 AGACCTTGTGTGTGTGTCGACAAAGAAATGATGAAAGATGATGCAATGAATATCACCA 937  
QY 392 hTyrValLeuThrIleLeuAsnMetValSerAlaLeuPheLysAsp----- 407  
Db 938 CTTACGCTGCTCAGATATCAACATGATGTTCTGTTATTAACAAGATGAAACAATAGAG 997  
QY 407 ----- 407  
Db 998 GAAACATCAACATTGCAATTGAGTCTGATTCCTTGAAGATGAACACGACGACTGG 1057  
QY 408 -----GlyLeuM 410  
Db 1058 TGAATAGTCAACGACGACACACCTTAAGTACGTTCTGCGACGTGCACTGGATTGA 1117  
QY 410 eGlyLysAspGlyThrArgHisAspHisAlaAlaIleLeuLeuThrGlyLeuAspIleCys 430  
Db 1118 TGGGGAAGATGGGACTCGTCATGACCAAGCCATCTTAAGTGTGCTGAGATATGTT 1177  
QY 430 eTTPrLysAsnGlnProCyAspThrLeuGlyPheAlaProIleSerGlyMetCysSerL 450  
Db 1178 CTTGGAAGATGAGCCCTGTGACACTTGGGATTTGCAACCCATTAAGTGAATGTGTGA 1237  
QY 450 YefTyrArgSerCysThrIleAsnGluAspThrGlyLeuGlyLeuAlaPheThrIleAlaH 470  
Db 1238 AATATGCAAGCTGCAAGATTAATGAAGATACAGGTCTTGAGCTGGCTTCAACATTTGCC 1297  
QY 470 iGluSerGlyHisAsnPheGlyMetIleHisAspGlyGluGlyAsnMetCysLysLys 490

Db 1298 ATGAGTCTGGACACAACTTTGGCATGATTCATGATGGAGAGGAAACATGTGAAAAAGT 1357  
QY 490 erGluglYasniIemSeSerProThrLeuAlaIyArGaenGlyValPheSerTrpSerP 510  
Db 1358 CCGAGGGCAACATCATGTCCTTACATTTGGCAGAGCAATGGAGTCTTCTCGGTGAC 1417  
QY 510 rOcYsSerArGlnTrpLeuHleYpHeLeuSerThraIagInAlaIleCYsLeuAla 530  
Db 1418 CTGGACGGCCGAGTCTACACAAATTTCTAGACACCGGTCAAGCTATCTGCTTGGCTG 1477  
QY 530 spGInProLySProValIyGluTrpGlyTrpGluYpLeuProGluYgluLeuTYrA 550  
Db 1478 ATGACGCCAAGCCTGTGAGGAATACAGATTCCTGAGAAATTTGCCAGAGAAATTATAG 1537  
QY 550 spAlaAnThrGlnCYsLYeTrpGlnPheGlygluYsAlaIyLeuCYmeLeuAsp 570  
Db 1538 ATGCAAAACACAGTCAGAGTGGCAGTTCCGAGAGAAAGCCAGACTCTGCATCTGAGACT 1597  
QY 570 helYalYasArpIleCYsLYeAlaLeuTrpCYeHleArGlnleGlyArGlyYsCYeGlnThrl 590  
Db 1598 TTAAGAAAGCATCTGTAAGCCCTGTGTGTCATGTATGGAGAAATGTGAGACTTA 1657  
QY 590 yArPheMeCProAlaAlaGluGlyThrlCYeCYsGlyHleAspMeCTrPYsArGlyGlyG 610  
Db 1658 AATTATTCAGCAGCAGAGAGCAAAATTTGTGGCATGACATGTGTGCGGGAGAGAC 1717  
QY 610 InCYsValIySyrGlyArPglYpLoYArProThrHleGlyHleSTrPSeArSPTrS 630  
Db 1718 AGTGTGTGAATGTGTGATGAGAGGCCCAAGCCCACTGCGCCTGCGAGCTGGT 1777  
QY 630 eArSeTrPSeArProCYsSerArGThCYsGlyglYsAlaIyLeuSerHleArGSeArGLeu 650  
Db 1778 CTTCCTGTGTCCTCATGCTCCAGGACCTGGAGAGGAGAGATCTCAAGAGTGCCTCT 1837  
QY 650 yArThzAnProLySProSeHleGlyGlyYpArPheCYsGluGlySerThraGThLeu 670  
Db 1838 GCACCAACCCCAAGCCATGSCATGGAGGAAGTTCTGTAGAGGCTCCATCCGACCTGA 1897  
QY 670 yArLeuCYsAnSeSerGlnLYsCYsProArGArPSeValArPheArGAlaIagInCYsA 690  
Db 1898 AGCTCTGCAACAGTCTGAAATGTCCCGGAGCAGTGTGCTCCGTGCTCAGTGTG 1957  
QY 690 lAgInHleAnSeSerArGArPheArGlyArGlnSTrYrLeuSTrPlyArProYrThrGlnY 710  
Db 1958 CCGAGCAACACAGCAGATTCATAGAGGGCGCATCAAGTGAAGCCTTACACTCAAG 2017  
QY 710 aGInuArPglInArPLeuCYsLYeLeuTYrCYsIleAlaGluGlyPheArPhePheS 730  
Db 2018 TGAAGATCAGGACTTATGCAAACTCTACTGTATCCAGAGAAATTTGATTTCTTTT 2077  
QY 730 erLeuSeArAnLYsValLYsArPGLYThrProCYsSerGluArPSeArArGaenValCYeI 750  
Db 2078 CTTCCTGCAATAAAGTCAAGATGAGACTTCATGCTCGAGGATACCCGTAATGTTGTA 2137  
QY 750 lArPArGlyIleCYsGlyuArGValGlyCYsArPAnValleuGlySeArAPAlaValGlnA 770  
Db 2138 TAGATGGATATGTGAGAGTTGATGAGACATGCTCTGGATGTAGTGCCTGTTGAAG 2197  
QY 770 spValCYsGlyValCYsArAnGlyAsnArPSeArIaCYeThrlHleIAsrGlyLeuTYrT 790  
Db 2198 AGCTCTGTGGGGTGTGAACGGGAATTACTCAAGCTCGCAAGANTTACAGAGGGCTTACA 2257  
QY 790 hleYHleHleHleSTrArPAnGlnTYrTYrHleMeValThrlleProSerGlyAlaArG 810  
Db 2258 CCAAGACCAACACCAACCAAGTATTAACAATGTGTCAACATTCCTTGTGGAGCCCGGA 2317  
QY 810 erIleArGlnIleTYrGluMeArPAnValSerThSerTYrIleSeValArGaenAlaLeuA 830  
Db 2318 GATTCGGCATCTATGAAATGAAGCTCTCACTCCATCAATTTCTGCGCAATGCCCTTA 2377  
QY 830 rGArGlyTYrLeuAnGlyHleSTrPThrValArPTrPProGlyArGlyLYsGlyAr 850  
Db 2378 GAAAGTACTACCTGATGGGCACTGAGCCTGTGACTGGCCGCGCGGTCAAAATTTTCCG 2437

QY 850 lYThrThrPheArPTrArGArGSeTYrAsnGluProGluAnLeuIleAlaThrlYp 870  
Db 2438 GCATTACTTTCAGTACAGACGGTCTTAATGAGCCCGAGAACTTAATCGCTACGAGAC 2497  
QY 870 rOTThrAsnGluThrLeuIleValGluLeuLeuPheGlnGlyArGAnPProGlyValAla 890  
Db 2498 CAACCAACGACGACATGATGTGAGAGCTGCTGTTCAGAGGAAGGAACCGGGGTGGCT 2557  
QY 890 rPGLuTYrSeMeCProArGLeuGlyThrlGluLYsGlnProProAlaGlnProSeTYrT 910  
Db 2558 GGGATTACTCCATGCTGCTGCTGGGAGCCGAGAACAGCCCTCGCCAGCCAGCTACA 2617  
QY 910 hTrPAlaIleValArGSeGluCYsSerValSerCYeGlyGlyArG 926  
Db 2618 CTGGGCGCATCGTGCGCTGTGAGTGTCTCGTCCGCGAGGGGAGACAG 2667

## RESULT 6

US-10-217-774-3  
/ Sequence 3, Application US/10217774  
/ Publication No. US20020193583A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Fiddie, Carl Johan  
/ APPLICANT: Hilpun, Erin  
/ TITLE OF INVENTION: No. US20020193583A1el Human Proteases and Polynucleotides Encoding  
/ TITLE OF INVENTION: Same  
/ FILE REFERENCE: LEX-0219-USA  
/ CURRENT APPLICATION NUMBER: US/10/217,774  
/ PRIOR FILING DATE: 2002-08-12  
/ PRIOR APPLICATION NUMBER: US/09/930,872  
/ PRIOR FILING DATE: 2001-08-14  
/ PRIOR APPLICATION NUMBER: US 60/225,852  
/ NUMBER OF SEQ ID NOS: 5  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 3  
/ LENGTH: 3675  
/ TYPE: DNA  
/ ORGANISM: homo sapiens  
US-10-217-774-3

## Alignment Scores:

Pred. No.:	0	Length:	3675
Score:	3981.50	Matches:	764
Percent Similarity:	78.26%	Conservative:	17
Best Local Similarity:	76.55%	Mismatches:	38
Query Match:	76.04%	Indels:	181
DB:	13	Gaps:	10

US-09-981-151D-8 (1-952) x US-10-217-774-3 (1-3675)

QY 1 MetLYsProArGAlaArGGLYrPArGlyLeuAlaAlaLeuTrpMeLeuAlaGln 20  
Db 1 ATGAAGCCCGCGCGCGAGATGGCGGGCTTGGCGCGCTGTGATGCTGTGGCGGAG 60  
QY 21 ValAlaGluGlnValSerProGlyArGSeHleGlnArGlyAsnArGlySerGlyGln 40  
Db 61 GTGGCCGAGCA----- 71  
QY 41 LeuGluAlaSerProProArGLeuLeuSerArGlyProArGArGLeuThrlaMetSer 60  
Db 71 ----- 71  
QY 61 ProLeuPheSerAlaGlyThrCYeValArGlnleGlyThrArGSeGlySerAlaTrpGln 80  
Db 72 -----GGACCTGGCGTGGCCATGGAGACCCGAGCGCGCTGGAG 116  
QY 81 ProGluArPProAlaSerSerSerThraGlyAlaAlaGlyLeuArPGLY-LYsGlyAr 100  
Db 117 CCGGAGCGTCCCGCTCTCTCCACCCGCGAGCGCGGGCTGGATGGAAAAAGGCG- 174  
QY 100 gArPheArGlnAlaGlyAsnHleArGSeGlnGlnThraAnThrlGlyThrlGluAnGln 120

Db 174 ----- 174  
Qy 120 nThrLeuNHValLeuThrGlnTyAAspLeuValSerAlaTyArgLysValAspHisArgI 140  
Db 175 -----GAAATGACGTGGTCTTGCTTACGAGGTTCACACAGGG 215  
Qy 140 yAspTyValSerHisGlnIleMetHisHisGlnArgArgArgAlaValAlaValSe 160  
Db 216 CGATTAGGTGCTCCATGAATTCATGACCATGACGGCGGAGAAAGACAGTGGCGGTCTC 275  
Qy 160 rGluValAGLLeuSerLeuHisValLeuArgLeuLysGlyProArgHisAspPheHisMetAspLe 180  
Db 276 CGAGGTGAGCTCTTCACCTTCGGCTGAAGAGCTCCAGGACACGATTCACAGGTGAGTCT 335  
Qy 180 yAspThrSerSerSerLeuValAlaProGlyPheHisValAGLThrLeuGlyLysThrGI 200  
Db 336 GAGGACTTCACGACGCTTACGTGGCTCTGGCTTTATTTGTGCAAGCTTTGGAAAGACAG 395  
Qy 200 yThrLysSerValAGLThrLeuProProGlyAspPheCysPheTyGlnLysLeuArg 220  
Db 396 CACTAAGTCTGTGACACTTACCGCCAGAGACTTGTGTTCTATCAAGGCTCTTTGGC 455  
Qy 220 gSerHisArgAspSerProSerHisGlyGlyLysPheCysGlyGlySerThrArgThrLe 240  
Db 456 ATCACAACAGAAACTCC--TCAGTGGCCCTTTCAACTCCGCAAGGCTTTCAGAGCATGAT 512  
Qy 240 yLysLeuCysAspSerGlnLysCysProArgAspSerValAspPheArgAlaAGLncY 260  
Db 513 ACAG-----ACAGAAAGGCAATTAATCTCTTAAGGCCACT 548  
Qy 260 yAlaGlnHisAspSerArgArgPheArgGlyArgHisGlyArgLysProTyArgThrGI 280  
Db 549 TCCTTCACACTCTCA-----TGAAA----- 570  
Qy 280 nValAGLValAspLeuCysLysLeuTyCysHisLe-AlaGlyGlyPheAspPhePhePheS 300  
Db 571 -----CTCGCAGAG----- 580  
Qy 300 xLeuSerAsnLysValLysAspGlyThrProCysSerGlnAspSerArgAsnValCysI 320  
Db 581 --CTGGCCAAAGCAAGCTCGCCAGTCCCAAGATCTGTACAAAGATCCACAGAGCCCATGC 638  
Qy 320 LeAspGlyLysCysGlyLeuSerValValSerThrSer-----AlaHis----- 334  
Db 639 TCCT-GGGGCCAGTGAAGGTCTGTGTACCTCAAGAGATGGAGTGGCATCAATCAACCC 697  
Qy 334 ----- 334  
Db 698 TGCACAGACGCACTTCGCTGGAGCTGCCAAGAAAGCAGCATTTCTGTGAAGACGCA 757  
Qy 335 -----MetProGlnProProLysGlnAspLeuPheHisLeuProAspGlyTyArgS 352  
Db 758 AGAAATACATGCCCCCAAGCTCCCAAGSAAAGACCTTCATCTTGCAGATGAGATTAAGT 817  
Qy 352 xCysLeuAspGlnHisLysArgSerLeuLeuArgSerHisArgAsnGlyGlyLeuAsnValG 372  
Db 818 CTTCCTTAAGCGCATTAAGCGCTCTTCTGAAGTCCCATAGAAATGAAGACTGAAGTGG 877  
Qy 372 LuThrLeuValValValAspLysLysMetGlnAsnHisGlyHisGlyAsnLLeThrT 392  
Db 878 AGACCTTGGTGGTGGTGCAGAAAGATGATGCAAAACCATGGCCATGAAATATCAACA 937  
Qy 392 hTrpTyValLeuThrHisLeuAspMetValSerAlaLeuPheLysAsp----- 407  
Db 938 CCTACGCTGTCAGATCTCAACATGGTATCTGTTATTCAAAGATGAAACAATAGAG 997  
Qy 407 ----- 407  
Db 998 GAAACATCAACATTGCAATTGTAGTGTGATTTCTTGAAGATGAACAGCCAGAGACTGG 1057  
Qy 408 -----GlyLeuH 410  
Db 1058 TGATTAAGTCAACAGCAGACACACTTAAGTAGCTTCTGCAAGTGGCACTGTGATTGA 1117

Qy 410 eCGLysAspGlyThrArgHisAspHisAlaAlaLeuLeuThrGlyLeuAspLysCysS 430  
Db 1118 TGGGAAAGATGGGACTCGTCATGACCAAGCCATCTTACTGACTGCTCGAATATGTT 1177  
Qy 430 eTrpLysAsnGlnProCysAspThrLeuGlyPheAlaProLysSerGlyMetCysSerL 450  
Db 1178 CCTGGAAGAAATGAGCCCTGTGACACTTGTGGATTTCCACCCATTAATGGAATGTGTAGTA 1237  
Qy 450 yThrArgSerCysThrHisAsnGlyAspThrGlyLeuGlyLeuAlaPheHisAlaHis 470  
Db 1238 AATATGCAAGCTGCAAGATTAAGATTAACAGGTCTTGACTGGGCTTCACCATATGCC 1297  
Qy 470 LeGlySerGlyHisAspPheGlyMetHisAspGlyGlyGlyAspMetCysLysLysS 490  
Db 1298 ATGAGCTGGAACAACATTGGCATATTCATGATGGAAGAGGAACATGTGTAAGTAAG 1357  
Qy 490 eCGLysLysAsnLLeMetSerProThrLeuAlaGlyArgAsnGlyValPheSerTrpSerP 510  
Db 1358 CCGAGGGCAACATCATGTCCCTTACATGGCAGAGACGCAATGAGATCTTCTCGGTGAC 1417  
Qy 510 rCysSerArgGlnTyArgLeuHisLysPheLeuSerThrArgAlaAlaLysLeuAla 530  
Db 1418 CTGCAAGCCGCGAGATTCACAAATTTCTAAGCACCGCTCAAGCTATCTGCTTGCTG 1477  
Qy 530 sPGLnProLysProValLysGlyTyArgLysTyProGlyLysLeuProGlyGlyLeuTyArg 550  
Db 1478 ATCAGCCAAAGCTGTGAAGGAATACAAATCTCTGAAGAAATTCAGAGAAATTAATG 1537  
Qy 550 sPGLAsnThrGlnCysLysTrpGlnPheGlyGlyLysAlaLysLeuCysMetLeuAsp 570  
Db 1538 ATCACAACACACAGTCAAGTGGCAGATTCGAGAGAAACCAAGCTCTGCATCTGGACT 1597  
Qy 570 hLysLysAspLysLysCysLysAlaLeuTrpCysHisArgGlyLeGlyArgLysCysGlyLThrL 590  
Db 1598 TTAAAGAGACATCTTAAGCCCTGTGGTCCATGTGATGAAGAAATGGAACATTA 1657  
Qy 590 yAspMetProAlaAlaGlyGlyThrLysCysGlyHisAspMetTrpCysArgGlyGlyG 610  
Db 1658 AATTATTCAGCAGACAGAAAGGACAAATTTGTGGCATGATGTGTGTCGGGAGAGAC 1717  
Qy 610 LncValLysTyArgLysAspGlyGlyProLysProThrHisGlyHisGlyTrpSerAspTrpS 630  
Db 1718 AGTGTGAAATGATGTGATGAAGGCCCAAGGCCCACTGAGTGGCTCGGACTGGT 1777  
Qy 630 eSerTrpSerProCysSerArgThrCysGlyGlyGlyValSerHisArgSerArgLeuLnc 650  
Db 1778 CTTCCTGTGCCCATCTCCAGGACCTCGGAGGGGAGATATCTCATAGGATGCGCTCT 1837  
Qy 650 yThrAsnProLysProSerHisGlyGlyLysPheCysGlyGlySerThrArgThrLeuL 670  
Db 1838 GCACCAACCCCAAGCCATGCGATGAGAGGAAGTCTGTGAGGGCTCATCTGCACTTGA 1897  
Qy 670 yLeuCysAspSerGlnLysCysProArgAspSerValAspPheArgAlaAlaGlnCysA 690  
Db 1898 AGCTTGCAACAGTCAAGAAATGCCCCGGGACAGTGTGACTTCGCTGCTCACTG 1957  
Qy 690 LeGlyHisAspSerArgArgPheArgGlyArgHisGlyTyArgLysTrpLysProTyArgThrGlnV 710  
Db 1958 CCGAGGACAAACAGCAACATTCAGAGGGCGGCACTACAAAGTGAAGCCTTACACTCAAG 2017  
Qy 710 ALGlyAspGlnAspLeuCysLysLeuTyCysHisLeaGlyGlyPheAspPhePheS 730  
Db 2018 TAGAATACAGACTTAATGCAACTTACTGTATTCGCAAGAAATTTGATTTCTTTT 2077  
Qy 730 xLeuSerAsnLysValLysAspGlyThrProCysSerGlnAspSerArgAsnValCysI 750  
Db 2078 CTTCGTCAATATAAGTCAAGATGGGACTCCATGCTCGAGGATACCGGAATGTTTGA 2137  
Qy 750 LeAspGlyLysCysGlyArgValGlyCysAspAsnValLeuGlySerAspAlaValGlnA 770  
Db 2138 TAGATGGATATGTGAGAGATTTGATGTGACAAATGTCTTGATCTGATGCTGTGAAG 2197







D 878 AGACCTTGTTGGTGGTCGACAAAAGATGATGCAAAACATGGCCATGAAAATATACCA 937  
Q hrTyValleuThrilleuAsnMetValserAlaLeuPheLysAsp----- 407  
D 392 hrTyValleuThrilleuAsnMetValserAlaLeuPheLysAsp----- 407  
D 938 CTTACGGTCTCAGATATCTCAACATGGTATCTGTTTATTCMAAGATGAAACAATAGAG 997  
Q 407 ----- 407  
D 998 GAAACATCAACATTGCAATTGAGTCTGATTCTTCTAGAAAGATGAACAGCCAGACTGG 1057  
Q 408 -----GlyLeuM 410  
D 1058 TGATAAGTCAACACGACGACACACCTTAAGTAGCTTCTGACAGTGGCACTGGATTGA 1117  
Q 410 etGlyLysAspGlyThrArgHisAspHisAlaIleLeuLeuThrGlyLeuAspIleCys 430  
D 1118 TGGGGAAAGATGGAGCTGTCATACCAAGCCATCTTACTGACTGGTCTGATATATGTT 1177  
Q 430 eTTPlyAsnGlyProCysAspThrLeuGlyPheAlaProIleSerGlyMetCysSerL 450  
D 1178 CTTGGAAGATGAGCCCTGTGACCTTTGGGATTGGACCCATAGTGAATGTGTAGTA 1237  
Q 450 ysrTyraSerSerCysThrIleAsnGlyAspThrGlyLeuGlyLeuAlaPheThrIleAla 470  
D 1238 AATATGCACTGCAAGATTAATGAAGATACAGGCTCTTGAGCTGGCCCTTCAACATTGCC 1297  
Q 470 fagLysSerGlyHisAsnPheGlyMetIleHisAspGlyGlyGlyLysAsnMetCysLys 490  
D 1298 ATGAGTCTGACACACATTTGGCATGATCTCATGATGAGAAAGGAAACATGTGTAAGT 1357  
Q 490 etGlyLysAsnIleMetSerProThrLeuAlaGlyArgAsnGlyValPheSerTrpSer 510  
D 1358 CCGAGGGCAACATCATGTCCCTTACATTGGCAGAGCCCAATGAGCTTCTCCGGTCA 1417  
Q 510 rocCysSerArgGlyTrpLeuHisLysPheLeuSerThrAlaGlnAlaIleCysLeuAla 530  
D 1418 CTTGCAAGCCCGCAGTATCTACAAATTTCTAAGCACCGCTCAAGCTATGTGCTGCTG 1477  
Q 530 spGlnProLysProValLysGlyLysTrpGlyTrpProGlyLysLeuProGlyLysLeu 550  
D 1478 ATCAGCCAAAGCTGTGAAGAAATACAGATCTCTGGAATTTGCCAGGAAATTATATG 1537  
Q 550 sraLAsnThrGlnCysLysTrpGlnPheGlyGlyLysAlaLysLeuCysMetLeuAsp 570  
D 1538 ATGCAAAACACACAGTGCAGTGGCAGTTCGAGAGAAAGCAAGCTCTGCATGTGACT 1597  
Q 570 helYblyAspIleCysLysAlaLeuTrpCysHisAlaGlyGlyCysGlyLysLeu 590  
D 1598 TTTAAAGGACATCTGTAAAGCCCTGTGTGCCATCTGATTTGAAAGAAATGTGAGACTA 1657  
Q 590 ysrPheMetProAlaAlaGlyGlyThrIleCysGlyHisAspMetTrpCysArgGlyGly 610  
D 1658 AATTATTCAGCAGCAGAAAGGCAATTTGTGGCAATGACATGTGTGTGCGGGAGAGAC 1717  
Q 610 lncysValLysTyGlyAspGlyGlyProLysProThrHisGlyHisLysTrpSerAspTrp 630  
D 1718 AGTGTGTGAATATGTGATGAAGGCCCAAGCCCAACCATGGCCATGGTCCGACTGCT 1777  
Q 630 etSerTrpSerProCysSerArgThrCysGlyGlyValSerHisArgSerArgLeu 650  
D 1778 CTTCTTGTGTCCTCATGTCTCAGAGCCTGCGAGGGGAGATATCTCATAGAGATGCGCTCT 1837  
Q 650 ysrThrAsnProLysProSerHisGlyGlyLysPheCysGlyGlySerThrArgThrLeu 670  
D 1838 GCACCAACCCCAAGCCATCCGATGAGAGAAATTTCTTGAAGGCTCCACTCGACTGA 1897  
Q 670 ysrLeuCyAsnSerGlnLysCysProArgAspSerValAspPheArgAlaAlaGlnCys 690  
D 1898 AGCTCTGCAACAGTCAAAATATGTCCTCCGGGACAGTGTGACTTCCGTCGCTCAGTGTG 1957  
Q 690 laGlyHisAsnSerArgArgPheArgGlyValArgHisLysLysLysTrpLysProTrpThrGln 710  
D 1958 CCGAGCAACACAGACGATTCAGAGGGGCGCACTCAAGTGAAGCCTTACACTCAAG 2017

Q 710 aGlyLysAspGlnAspLeuCysLysLeuTrpCysIleAlaGlyPheAspPhePhe 730  
D 2018 TAGAAGATCAGGACTTATGAAACTCTACTGTATCCAGAGGATTTGATTTCTTCTTT 2077  
Q 730 etLeuSerAsnLysValLysAspGlyThrProCysSerGlyLysAspSerArgAsnValCys 750  
D 2078 CTTGTCAATTAATTAAGTCAAAAGATGGAGCTCCAGTCCGAGGGATACCCGTAAGTGTGA 2137  
Q 750 leAspGlyIleCysGlyLysValGlyCysAspAsnValLeuGlySerAspAlaValGly 770  
D 2138 TAGATGGATATGTGAAGATGTGAATGACATATCTTGGATCTGATGCTGTGAAG 2197  
Q 770 sraValCysGlyValCysAsnGlyAsnAsnSerAlaCysThrIleHisArgGlyLeuTrp 790  
D 2198 AGCTGTGGGGGTGTAAAGGAAATACCTCAGCTCGACAGATTCACAGGGGTCTTAC 2257  
Q 790 hrLysHisHisHisThrAsnGlnTrpThrHisMetValThrIleProSerGlyAlaArg 810  
D 2258 CCAAGCACCAACACACAAACAGTATTAACATGTGTACATCTCTTGTGAGCCCGA 2317  
Q 810 etIleArgIleTyrglyMetAsnValSerThrSerTyrlleSerValArgAsnAlaLeu 830  
D 2318 GTATCCGACATTAATGAATGAACGTCTTACCTCTACATTTCTGTGCGCAATGCCCTCA 2377  
Q 830 rgaTGTyTyLeuAsnGlyHisTrpThrValAspTrpProGlyArgTyTyLysPheSer 850  
D 2378 GAGGTATCTACCTGAATGGGCACTGACCGTGGACCTGGCCGGCGGTCAAAATTTTCG 2437  
Q 850 lYThrThrPheAspTyraArgSerTyraAsnGlyProGlyLysLeuIleAlaThrGly 870  
D 2438 GCACCTCTTGCAGCTCAGACGGCTCTTATATAGCCCGAGAACTTAATCGCTACGAGC 2497  
Q 870 rocThrAsnGlnThrLeuIleValGlyLeuPheGlnGlyArgAsnProGlyValAla 890  
D 2498 CAACCAACGAGACATGATGTGAGACTGTCTTGAAGGAAAGCCGGAGTGTGCT 2557  
Q 890 rpsLysSerMetProArgLeuGlyThrGlyLysGlnProProAlaGlnProSerTyTr 910  
D 2558 GGGAAATATCTCAGCTCGCTTGGGAGCCGAGAGAGGCCCTGCGCAAGCCAGCTTAC 2617  
Q 910 hrTPAlaIleValArgSerGlnCysSerValSerCysGlyGlyArg 926  
D 2618 CTTGGGCCATCTGCGCTCTGAGTCTCGGTGCTCGGAGGGGAGCAG 2667

RESULT 8  
US-10-804-457-3  
; Sequence 3, Application US/10804457  
; Publication No. US2005006534A1  
; GENERAL INFORMATION:  
; APPLICANT: Friedle, Carl Johan  
; APPLICANT: Hilbun, Erin  
; TITLE OF INVENTION: Novel Human Proteases and Polynucleotides Encoding the  
; TITLE OF INVENTION: Same  
; FILE REFERENCE: LEX-0219-USA  
; CURRENT APPLICATION NUMBER: US/10/804,457  
; CURRENT FILING DATE: 2004-03-19  
; PRIOR APPLICATION NUMBER: US/10/217,774  
; PRIOR FILING DATE: 2002-08-12  
; PRIOR APPLICATION NUMBER: US/09/930,872  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: US 60/225,852  
; PRIOR FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PaSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 3675  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-804-457-3  
Alignment Scores: 0 Length: 3675  
Pred. No.:

Score:	3981.50	Matches:	764
Percent Similarity:	78.26%	Conservative:	17
Best Local Similarity:	76.55%	Mismatches:	38
Query Match:	76.04%	Indels:	181
DB:	21	Gaps:	10
US-09-981-151d-8 (1-952) x US-10-804-457-3 (1-3675)			
QY	1	MetLysProAlaArgGlyTPAArgGlyLeuAlaLeuTrpMetLeuLeuAlaGln	20
DB	1	ATMAACCCCGCGCGCGGATGGCGGCTTGCGCGCTGTGATGCTGCGCGCAG	60
QY	21	ValAlaGlnGlnAlaSerProGlyArgSerHisGlnArgGlyAsnArgGlySerGlyGln	40
DB	61	GTGGCCGAGCA-----	71
QY	41	LeuGluAlaSerProProAlaLeuLeuSerArgGlyProArgArgLeuThrAlaMetSer	60
DB	71	-----	71
QY	61	ProLeuPheSerAlaGlyThrCysValArgHisGlyThrArgSerGlySerAlaATPGlu	80
DB	72	-----GGCACTGCGCGCGCATGGAGCCGCGCAGCGCGCGCGCTGGAG	116
QY	81	ProGluArgProAlaSerSerSerThrArgGlyValAlaGlyLeuAspGly-LysGlyArg	100
DB	117	CCGAGCGCTCCCGCTCTCTCCACCCGCGAGCGCGCGCTGTAGTGAAGAGGCG--	174
QY	100	GAPMeCAspGluAlaGlyAsnHisArgSerGlnGlnThrAsnThrGlyThrGluAsnGly	120
DB	174	-----	174
QY	120	nThrLeuHisValLeuThrGlnIleTyraPheLeuValSerAlaTYrGluValAspHisArgGly	140
DB	175	-----GAATATGACCTGGTCTCTGCTGCTACGAGATTGACCAACAGCGG	215
QY	140	YAspTYrValSerHisGluIleMetHisHisGlnArgArgArgArgAlaValAlaAlaSer	160
DB	216	CGATTACGGTCCCAAGAAATCATGCAACATCAGCGCGAGAAAGCAGTGGCCGTGTC	275
QY	160	rgLysValGluSerLeuHisLeuArgLeuLysGlyProArgHisAspPheHisIleMetAspLe	180
DB	276	CGAGGTGAGTCTCTTCACTTCGGCTGAAGGCTCCAGGCAAGCATTTCCACGTGATCT	335
QY	180	UArgThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrGly	200
DB	336	GAGGACTTCAGCAGCGCTAGTGGCTCTGGCTTATTTGTGCAGACGTTGGAAAGACAG	395
QY	200	YThrLysSerValGlnThrLeuProProGluAspPheCysPheTYrGlnGlySerLeuArg	220
DB	396	CACTAAGTCTGTGCACATTTACCGCAGAGGACCTTCTGTCTATCAAGGCTCTTTGGC	455
QY	220	GSerHisArgAsnSerProSerHisGlyGlyLysPheCysGluGlySerThrArgThrLe	240
DB	456	ATCACACAGAAACTCC--TCAGTGGCCCTTTCAACTGCACAGGCTTTCAGGCATGAT	512
QY	240	UlyValLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaAlaGlnCys	260
DB	513	ACGA-----ACAGAAAGAGCAGATTACTTCTTAAGGCGCACT	548
QY	260	AlaGlnHisAsnSerArgArgPheArgGlyArgHisTYrLysIleProTYrPheProTYrThrGly	280
DB	549	TCCTTACACCTCTCA-----TGGAAA-----	570
QY	280	nValGluAlaAspLeuCysLeuLeuTYrCysIle-AlaGluGlyPheAspPhePhePheS	300
DB	571	-----CTCGGCGAGAG-----	580
QY	300	eLeuSerAsnLysValLysAspGlyThrProCysSerGlyAspSerArgAsnValCysI	320
DB	581	--CTGGCCCAAGCGAGCTGCCATCCCACTACTGTACAAGAGATCCACAGAGCCCATGC	638
QY	320	LeaSpGlyLysCysGluLeuSerValValSerThrSer-----AlaHis-----	334

DB	639	TCCT--GGGCGCAGTAGAGTCTGTGTACCTCAAGGACATGGAGCTGGCACATCAACCC	697
QY	334	-----	334
DB	698	TCGACAGCAGCAGCCTTGCCCTGGGAGCTGCCAAGAAAGCATTTCTGTGAAGACGCA	757
QY	335	-----MetProGlnProProLysGluAspLeuPheIleLeuProAspGlyTYrLys	352
DB	758	AGAAATACATGCCCCAGGCTCCCAAGGAAAGACCTTCACTTTCGACATGTAGTAAAGT	817
QY	352	eCysLeuAsnArgHisLysValArgSerLeuLeuArgSerHisArgAsnGlyGlnLeuAsnValG	372
DB	818	CTTGCTTACGGCATTAAGGCTCTCTTCTGAGGTCCTCATAGAATGAATGAAGAACTGAAC	877
QY	372	IuThrLeuValValAlaAspLysLysMetMetGlnAsnHisGlyLysIleAsnIleThrT	392
DB	878	AGACCTTGCTGGTGGTCCAGCAAAAAGATGCAAAACATGCGCATGAAATATCACACA	937
QY	392	hTYrValLeuThrIleLeuAsnMetValSerAlaLeuPheLysAsp-----	407
DB	938	CTTACGTGCTCAGTACTCAACATGTATCTGCTTTATTCAAAGATGGAACAATAGAG	997
QY	407	-----	407
DB	998	GAAACATCAACATTGCAAATTGTAGTCTGATTTCTTAGAAGATGAACACCGAGACTGG	1057
QY	408	-----GlyLeuM-----	410
DB	1058	TGATAAAGTACACGAGCAGACCAACCTTAAGTACTTCCGCAAGTGGCAGTGTGATTGA	1117
QY	410	eGlyLysAspGlyTYrArgHisAspHisAlaIleLeuLeuThrGlyLeuAspIleCysS	430
DB	1118	TGGGAAAGATGGGCTGCTGTCATGACCAAGCATCTTACTGACTGCTGGATATATGTT	1177
QY	430	eTYrLysAsnGluProCysAspThrLeuGlyPheAlaProIleSerGlyMetCysSerL	450
DB	1178	CTGGAAAGATGAGCCCTGTGACATTGGGATTTGGACCCCATTAAGTGAATGATGATGA	1237
QY	450	YsTYrArgSerCysThrIleAsnGluAspThrGlyLeuGlyLeuAlaPheThrIleAlaH	470
DB	1238	AATATCGCAGCTGCACGATTAATGAAGATACAGGCTTGGACTGGCTTTCACCATTTGCC	1297
QY	470	IeGluSerGlyHisAsnPheGlyMetIleHisAspGlyGluGlyLysAsnMetCysLysLys	490
DB	1298	ATGACTCTCGACACCACTTTGGCATGATTCATGAAGGAGGAAACATGTCTAAATAAGT	1357
QY	490	eGluGlyAsnHisIleMetSerProThrLeuAlaGlyArgAsnGlyValPheSerTrpSerP	510
DB	1358	CCGAGGCGACATCATGTCCCTTACATTGGCAGGAGGCAATGGAATCTTCTCTGGTCA	1417
QY	510	roCysSerArgGlnTYrLeuHisLysPheLeuSerThrAlaGlnAlaIleCysLeuAla	530
DB	1418	CTGCAGCGCGCAGTATCTACCAAAATTTCTTAAGCAGCGCTCAAGCTATCTGCTTGG	1477
QY	530	sPrlnProLysProValLysGlyTYrLysTYrProGluLysLeuProGlyGluLeuTYrA	550
DB	1478	ATCAGCCAAAGCGTGTGAAGAAATTAAGATATCCGAAATAATGGCAGAGAAATTAATG	1537
QY	550	sPAlaAsnThrGlnCysValTYrTrpGlnPheGlyGlyLysAlaLysLeuCysMetLeuAspP	570
DB	1538	ATGCAAAACACACAGTGCAGAGTGGCAGTTTCGAGAGAAAGCCAAAGCTTGCATGCTG	1597
QY	570	hLysLysAspIleCysLysAlaLeuTrpCysHisArgIleGlyArgLysCysGluThrL	590
DB	1598	TTAATAAGACATCTGTAAAGCCGTGTGTCATCGTATTTGAAGAAATGTGAGACTA	1657
QY	590	YsPheMetProAlaAlaGluGlyThrIleCysGlyHisAspMetTrpCysArgGlyGlyG	610
DB	1658	AATTTATCCGACGACAGCAAGAGCACAATTTGTGGGCATGAGATGTGGTCCGGGAGAG	1717
QY	610	IuCysValLysTYrGlyAspGlyProLysProThrHisGlyHisTYrPheSerAspTrpS	630

```
Db 1718 AGTGTGTAATATGTGATGAAGCCCAAGCCCACTGGCTGGTGGTGGT 1777
Qy 630 eSertPserProCySeSerArgThrCySglYglYValSerHisArgSerArgLeuc 650
Db 1778 CTTCTTGCTCCCACTGCTCCAGACCTGCGAGGGGAGATCTCATAGAGTCCCTCT 1837
Qy 650 yaThraenProLyPserSerHisaglYglYlyPheCySglYglYSerThrArgThreul 670
Db 1838 GCACCAACCCCAAGCCATCCATGAGGAGGAAGTTCTGTGAGGGGCTCCAGCTCTGA 1897
Qy 670 yaleuCySaenSerGlnlyCySeProArgPheSerValaAppheArgAlaaglncysa 690
Db 1898 AGCTGTGCAACAGTCAGCAAAATGTCCTCCGGGACAGATGTGACTTCCTCCAGTGTG 1957
Qy 690 laGlunHisaenSerArgArgPheArgglYArgHisrYlySTpLyPProYThrGlnY 710
Db 1958 CCGAGCAACACAGACGACGATTCAGAGGGGCGCATCAAGTGGAGCCCTTAACCTAG 2017
Qy 710 aiglunepglnaAppLeuCySlyaleuYrCySllleaglYglYpheaApphePheS 730
Db 2018 TAGAAGATCAGGACTTATGCAAACTTACTGTATCCGAGAAGGATTTGATTTCTCTTT 2077
Qy 730 erLeuSeranlyValyValaAppglYThrProCySeSerGluAppSerArgAsnValCysl 750
Db 2078 CTTTGTCAAATTAAGTCMAAAGATGGGACTCCATGCTCGAGAGATAGCCCTAATGTTGTA 2137
Qy 750 leaepgLyIeCySglunArgValglYCySaPaenValleuGlySerAspAlaValglun 770
Db 2138 TAAATGGGATATGTGAAGAGTGTGATGTGACAAATGCTTGAGTCTTGAGTGGTGAAG 2197
Qy 770 spValCySglYValCySaenGlyAsaPaenSerAlaCySthrlleHisArgglYleuYrT 790
Db 2198 ACCTGTGGGGGTGTGTAACGGGAATACCTCAGCTGTCACAGATTCAAGGGGCTCTACA 2257
Qy 790 hrlYshshshshThraenGlnYrYrHismeValThrllleProSerGlyAlaArgS 810
Db 2258 CCAAGCACCAACACACACAGATATATCATAGTGCACCATTCCTTCTGAGGCCGGA 2317
Qy 810 erlleargLyIeYrGluMeAsnValSerTherSerYrllleSerValArgAsnAlaLeua 830
Db 2318 GTATCCGACATCTAAGAAATGAACGTCTACCTCTACATTTCTGTGCGGAAGCCCTCA 2377
Qy 830 rgaYrYrYrYleuAsnGlyHisrThraValaAppTrProglYArgYrYrYrPheSerg 850
Db 2378 GAAGGATACCTACCTGAATGGGACATGACCGTGGACTGGCCGGTCAAAATTTTCGG 2437
Qy 850 lyThrThraPheAppYrYrArgArgSerYrAenGluProgluAsnleuAlaThrGlyP 870
Db 2438 GCACTACTTTCGACTACAGACGGCTCTATATAGGCCCGGAACCTTAATGCTACCTGAC 2497
Qy 870 roThraenGluThrleuAlleValgluLeuPheGlnGlyArgaenProglYValaIaT 890
Db 2498 CAACCAACGAGACCTGATGTGAGCTGCTTCAAGGAGGAAGAACCCGGGTGGTCCCT 2557
Qy 890 rpglYrYrSerMetProArgLeuGlyYrThrlYrYrGlnProProAlaGlnProSerYrT 910
Db 2558 GGGAAATACCTCAGTCCCTCGCTTGGGAGACGAGAAAGACCCCTCGCCCAACGAGCTACA 2617
Qy 910 hrTrpAlaAlleValaJrSerGluCySeSerValSerCySglYglYglYArg 926
Db 2618 CTGGGGCATCTGTGCGCTGTGAGTGTCTCGTGTCTTCGAGGGGGGAGCAG 2667

RESULT 9
US-10-217-774-5
; Sequence 5, Application US/10217774
; Publication No. US20020193583A1
; GENERAL INFORMATION:
; APPLICANT: Fiddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. US20020193583A1 Human Proteases and Polynucleotides Encodit
; TITLE OF INVENTION: Same
; CURRENT APPLICATION NUMBER: US/10/217, 774
```

```
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/930, 872
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225, 852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4042
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-774-5

Alignment Scores:
Pred. No.: 0 Length: 4042
Score: 3981.50 Matches: 764
Percent Similarity: 78.26% Conservative: 17
Best Local Similarity: 76.55% Mismatches: 38
Query Match: 76.04% Indels: 181
DB: Gaps: 10

US-09-981-151D-8 (1-952) x US-10-217-774-5 (1-4042)

Qy 1 MetLyseProArgAlaArgglYrPArgglYleuAlaAlaLeuTrpMetLeuAlaGln 20
Db 99 ATGAAGCCCGCGCGCGGATGGCGGGCTTGGCGGCGCTGGATGCTGTCGGCGAG 158
Qy 21 ValAlaGluGlnValSerProglYArgSerHisGlnArgglYAsnArgglYSerGlyGln 40
Db 159 GTGGCCGAGCA----- 169
Qy 41 LeuGluAlaSerProArgLeuLeuSerArgglYProArgArgLeuThrAlaMetSer 60
Db 169 ----- 169
Qy 61 ProLeuPheSerAlaGlyYrCySValaArgHisglYThrArgSerGlySerAlaTrpGlu 80
Db 170 -----GGCACTGCGTGGCGCATGGGAGCCGCGAGCCGCGCGCTGGAG 214
Qy 81 ProGluArgProAlaSerSerSerThraArgglYAlaAlaGlyleuAspGlyLySglYArg 100
Db 215 CCGAGACGTCGCGCGTCTCTTCACACCGCGAGCGCGCGGTGATGGAAGAGGCGC-- 272
Qy 100 gaPmetAspGluAlaGlyAsnHisArgSerGlnGlnThraenThrGlyYrThrGluAsnG 120
Db 272 ----- 272
Qy 120 nThrleuHisValleuThrGlnYrAspLeuValSerAlaYrGluValaAspHisArggl 140
Db 273 -----GAATATGACCTGGTCTCTGCTACAGAGTTGACACAGAGG 313
Qy 140 yaPArgYrYrValSerHisGlnllleMetHisrGlnaGagaGArgAlaValaIaSe 160
Db 314 CGATTACGTGTCCCAAGAAATCATGCACATCAGCGCGAGAAAGACAGTGGCCGTGTC 373
Qy 160 rglValaGluSerLeuHisleuArgLeuYrSglYProArgHisAspPheHismeAspLe 180
Db 374 CAGAGTTAGTCTCTTACACTTGGCTGAAAGGCTCAAGGACGACTTCCACCTGATCT 433
Qy 180 uArgThraSerSerSerLeuValaIaProglYPheIleValaGlnThrleuGlyYrThrl 200
Db 434 GAGGACTTCAGACGCTAGTGGCTCTCGCTTATTTGACAGACCTTGGGAAAGACAG 493
Qy 200 YrThrlYrSerValaGlnThrleuProProgluAppPheCySPherYrGlnGlySerleuArg 220
Db 494 CACTAAGTCTGTGACAGACTTACCCGCAAGAGACTTCTGTTCTTACAGAGCTCTTGTGG 553
Qy 220 gSerHisArgaenSerProSerHisaglYglYlyPheCySglunGlySerThrArgThre 240
Db 554 ATACACAGAAACTCC---TCACTGGCCCTTTCAACCTGCCAAGGCTTGTCAAGCATGAT 610
Qy 240 uYrleuCySaenSerGlnlyCySeProArgPheSerValaAppheArgAlaAlaaglncY 260
Db 260 -----
```

Db 611 AGCA-----ACAGAGGCGAGATTACTTCTTAAGCCACT 646  
Qy 260 sAlaGluHIsaenSerArgRpheargGlyArgHIsTyRlyeRPrOlyrThrG1 280  
Db 647 TCCTTCACACCTCTCA-----TGAAA-----668  
Qy 280 nValGluIaAspLeuCylLeuTyRcyS11e-ALaGluGlyRheAspRhePhePhes 300  
Db 669 -----CTCGGCAGAG-----678  
Qy 300 eRLeuSerAsnLyVaLyAspGlyThRProCySseRglYAspSerArgAsnValCyel 320  
Db 679 --CTGCCCAAGGAGAGCTCGCCATCCCATGTACTGTACAGAGATCCAGAGGCCCATG 736  
Qy 320 LeAspGlyIleCyBgIuLeuSerValIaSerThRser-----AlaHis-----334  
Db 737 TCCT-gGGGCGAGTGAAGTCTGTGACCTCAAGACATGGGAGCTGGACATCAACCCC 795  
Qy 334 -----334  
Db 796 TGCACAGACGCACTTCGCTGGAGCTGCACAAAGACGATTTCTGTGAAGAAGCA 855  
Qy 335 -----MetProGlnProProLyGluAspLeuPheIleLeuProAspGluTyRlyes 352  
Db 856 AGAAATATACATGCCCGCAGCTCCCAAGAGAGACCTTTCATCTTGCCAGATGAGTAAAG 915  
Qy 352 eRcYLeuHArgHIsLyBaRgSerLeuLeuArgSerHIsaRgAsnGluIuLeuAsnValG 372  
Db 916 CTTCGTTACGGCATTAAGCGCTCTTCTGAGGTCCTCATGAATGAAGAATCGAACTGG 975  
Qy 372 LuThRLeuValValIaAspLyLyMeMeRcGlnAsnHIsaGlyHIsGluAsnIleThR 392  
Db 976 AGACCTTGGTGGTGTGCGACAAAGATAGTCAAAACATGGCCATGAAATATCACCA 1035  
Qy 392 hRtyRValIeuthRiIleLeuAsnMetValSerAlaLeuPheLyAsp-----407  
Db 1036 CCAACGCTGCACGATACCAATGTAATCTGCTTATTCAAGATGAAACATAGAG 1095  
Qy 407 -----407  
Db 1096 GAAACATCAACATTGCATTGTAGTCTGATTTCTTAGAAGATGAACAGCCAGACTGG 1155  
Qy 408 -----GlyLeuM 410  
Db 1156 TGAATAAGTACCAAGGAGACCAACCTTAAGTACTTGCAGTGGAGCTGGAATTGA 1215  
Qy 410 eRcGlyLyAspRgLyThRArgHIsaRPHIsaAlaIleLeuLeuThRgLyLeuAspIleCyS 430  
Db 1216 TGGGGAAGATGGGACTCGTCATGACCAAGCCATCTTACTGAGTGTCTGGATATATGT 1275  
Qy 430 eRTrLyAsnGluProCyAspThRLeuGlyPheAlaProIleSerGlyMetCySserL 450  
Db 1276 CCTGGAAGATGAGCCCTGTGACACTTTGGGATTTGCACCCATAGTGAATGTGAAGA 1335  
Qy 450 yRtyRArgSerCySthRiIleAsnGluAspThRgLyLeuGlyLeuAlaRhetRiIleAlaH 470  
Db 1336 AATATGCAAGCTGCAGATTAATGAAGATACAGGTTTGAAGCTTGAGCTTCACCATGGCC 1395  
Qy 470 IeGlyuSerGlyHIsaenPheGlyMetIleHIsaRgLyGluGlyAsnMetCySlyLyS 490  
Db 1396 ATGAGCTTGGACACCACTTTGGCATATTCATGATGAGAGAGGAACATGTGTAAAAAT 1455  
Qy 490 eRtGluGlyAsnIleMetSerProThRLeuAlaGlyArgAsnGlyValPheSerTrpSerP 510  
Db 1456 CCGAGGGCAACATCATGTCCCTACATTTGGCAGAGCGCAATGGAGTCTTCCTGTGTAC 1515  
Qy 510 rOcYsSerArgGlnTyRLeuHIsLyRPhLeuSerThRAlaGlnAlaIleCyBgLeuAla 530  
Db 1516 CcTGACGCGCGAGATCTACACAAATTTCTAAGACCGCTCAAGCTATCTGCTTGCG 1575  
Qy 530 sRGLnProLyAspProValIyBgLyTyRlyeTyRProGluLyLeuProGlyGluLeuTyR 550  
Db 1576 ATCAGCCAAAGCCTGTGAAGGAATACAAATTCCTGAGAAATTTGCCAGAGAAATTAATG 1635

Qy 550 sPAlaAsnThRGlncYsLySTrpGlnPheGlyGluLyAlaLyLeuCyMetLeuAsp 570  
Db 1636 ATGCAAAACACAGATGCAAGTGGCAGTTCCGAGAGAAAGCCAAAGCTCTGCATGCTGACT 1695  
Qy 570 hElyLyLeuAspIleCyBgLyAlaLeuTrpCyS11eArgGlyGlyArgLySgGluThL 590  
Db 1696 TTTAAAGGACATCTGTAAAGCCTGTGTGTCATGTAAGGAAGAAATGTGAGACTA 1755  
Qy 590 yRPhMetProAlaIaGluGlyThRiIleCySgLyHIsaRmetTrpCyAsRgLyGlyG 610  
Db 1756 AATTTATGCCAGACACAAAGGACAAATTTGTGGCATGACATGTGTGCCGGAGAGAC 1815  
Qy 610 InCyValLySgLyAspGluGlyProLyRProThRHiagLyHIsaRTrpSerAspTrPS 630  
Db 1816 AGTGTGTAATATATGTGATGAAGGCCCAAGCCCAAGCCCATGCGCATGTGTGCACTGGT 1875  
Qy 630 eRSeRTrpSerProCySseRArgThRCyBgLyGlyGlyValSerHIsaRgSerArgLeu 650  
Db 1876 CTTCCTTGTCCTCCATGCTCCAGAGCTTCGGAGCGGAGGTATCTCATAGAGTCCCTCT 1935  
Qy 650 yRThAsnProLyRProSerHIsaGlyLyRPhCySgLyGlyYseRThRArgThRLeuL 670  
Db 1936 GCAACCAACCCAGGCAATCGCATGGAGGAAGTTCTGTAGGGCTCCACTGCACTTCA 1995  
Qy 670 yRLeuCyAsnSerGlnLyCySProArgAspSerValAspRheArgAlaIaGlnCyS 690  
Db 1996 AGCTGTGCAACAGTCAGAAATGTCCCGGGAACAGTTGACTTCGCTGCTCAGTGTG 2055  
Qy 690 IaGluHIsaenSerArgRpheargGlyArgHIsaTyRlyeRPrOlyrThrRglnv 710  
Db 2056 CCGACACAAACGACGACGATTCAGAGGCGGCACTCAACAGTGAAGGCTTACACTCAAG 2115  
Qy 710 aLGlAspGlnAspLeuCySlySLeuTyRcyS11eAlaGluGlyPheAspRhePhePhes 730  
Db 2116 TAGAAGATCAGGACTTAATGCAAACTGTATGTGACGAAGAGATTGATTTCTTCTTT 2175  
Qy 730 eRLeuSerAsnLyVaLyAspGlyThRProCySseRglYAspSerArgAsnValCyS 750  
Db 2176 CTTCGTCAAAATTAAGTCAAGATGGGACTCCATGCTCGAGAGATGCGGTAAATGTTTGA 2235  
Qy 750 LeAspGlyIleCyBgLyArgValGlyCySAspAsnValLeuGlySerAspAlaValGlu 770  
Db 2236 TAGATGGATATGTAGAGAGTGTGATGTGACAAATGCTTGGATCTATGTGTGAAG 2295  
Qy 770 sPValCySgLyValCySAsnGlyAsnAsnSerAlaCySthRiIleHIsaRgLyLeuTyR 790  
Db 2236 AGCTGTGTGGGTGTGAACGGGAATATCTAGCTGCACGATTCACAGGGGTCTTACA 2355  
Qy 790 hRtyRHiHIsaThRAsnGlnTyRHiSmetValThRiIleProSerGlyAlaArgS 810  
Db 2356 CCAAGCACACACACCAACAGTATATCAATGTGACCAATTCCTTCTGGAGCCCGGA 2415  
Qy 810 eRtLeArgIleTyGluMetAsnValSerThRserTyRiIleSerValArgAsnAlaLeu 830  
Db 2416 GTATCCGATCTATGAATGAACGCTCTACCTCTTAATTTCTGTGGCAATGCCCCCA 2475  
Qy 830 rGArgTyRtyRLeuAsnGlyHIsaRThRValAspTrpProGlyArgTyRlyRPhSerG 850  
Db 2476 GAAGTATCTACTGAATGGGCACTGACCGGTGACCTGGCCCGCGGTACAAATTTTGG 2535  
Qy 850 IyThRThRPhAspTyArgArgSerTyRAsnGluProGluAsnLeuIleAlaThRgLyP 870  
Db 2536 GCACACTTTTGCATACAGAGCGTCTTAATGAGCCCGAAGAACTTAATCGCTACGGAC 2595  
Qy 870 roThRAsnGluThRLeuIleValGluLeuLeuPheGlnGlyArgAsnProGlyValAlaT 890  
Db 2596 CAACCAAGACAGCATGATGTGAAGCTGCTGTTCAAGGAAGGAACCCGGGTGTGTGCT 2655  
Qy 890 rPGluTyRSeRmetProArgLeuGlyThRgLyLySglnProProAlaGlnProSerTyR 910  
Db 2656 GGAATATCTCATGCTGCTTGGGGACCGAAGAGAGCCCCCTGCCAGCCAGCTTACA 2715



Db 1336 AATATGCACTGACGATTAAATGAAGATACAGGCTTGAGCTGGCCCTTCAACCATTTGCC 1395  
Qy 470 IAGIUSERG1YH1SAENPHEGLYMEI1EH1SAPGLYGLUGLYAENMECYSLYELYS 490  
Db 1396 ATGAGTCTGGACACAATTGGCATGATTCATGATGGAAGAGGAAACATGTGTAAAAAGT 1455  
Qy 490 ERGLUGLYAENI1EMETSERPROTHLEUA1AGLYARGANGLYVALPHESERTIPSE 510  
Db 1456 CCGAGGGACACACATGATCCCTCACTGACAGAGCAATGAGATCTCTCTGCTGAC 1515  
Qy 510 ROCYSESERARGGLNYRLEUHI1ELYS PHEUSERTHR1AG1NALAI1EYSL1EUA1A 530  
Db 1516 CCGACGACCCGCGCATCTTACACAAATTTCTAAGCACCGCTCAAGCTATCTGCTTGCG 1575  
Qy 530 BPGLNPROLYSPROVALYVGLUTYR1YR1EYR1PROGLULYLEUPROGLYGLUL1EUTY 550  
Db 1576 ATCAGCCAAAGCCTGTGAAGAAATACAGATCTCTGAGAAATTTGCCAGAGAAATTTATG 1635  
Qy 550 SPALASANTHRG1N1CYSLYESTRPG1NPHG1YGLULYVALYLSLEUCYEMETLEUAPP 570  
Db 1636 ATGCACCAACACACAGTCAAGTGGCAGTTGGAGAGAAAGCAAGCTCTGCATGCTGACT 1695  
Qy 570 HELYELYSAP11EYSLYSA1ALEUTR1CYSH1SARG11EGLYARGLYSCYGLUTHTL 590  
Db 1696 TTTAAAAGACATCTTAAAGCCCTGTGTCATCTGATTGGAGAAATGTGAGACTA 1755  
Qy 590 YAPHEWETPRO1A1AG1UGLYTHR11EYSG1YH1SAPWETTR1CYSA1RGLYGLY 610  
Db 1756 AATTTATGCAGCAGACAGAAAGCACAAATTTGTGGCATGACATGTGTGTCGGGAGAGAC 1815  
Qy 610 INCYVALYSTRYR1YAPRGLUGLY1PROLYSPROTHR1H1AG1YH1STRPSEAPTRPS 630  
Db 1816 AGTGTGTGAATGTGTGATGAAGGCCCAAGCCCAAGTGGCCCACTGCTGACTGTGT 1875  
Qy 630 ERSETRIPSETR1CYSESERARGTH1CYSG1YGLYGLYVALSERH1SARGSERARGLEUC 650  
Db 1876 CTTCTTGCTGCCATCTCCAGSACCTGCGAGGGGAGATCTCTAAGAGTCCGCTCT 1935  
Qy 650 YETHRANPROLYSPROSERH1AG1YGLYVAPHECYSG1UGLYSERTHRARGTHLEUL 670  
Db 1936 GACACCAACCCCAAGCCATCGCATGAGAGGAAGTTCTGTAGAGGCTCCATCGCACTCTGA 1995  
Qy 670 YLEUCYSAENSERGLULYSCYSPROARGASPER1AL1APHPHEARG1A1AG1NCYVA 690  
Db 1996 AGCTCTGCACAGTCAAGAAATGCCCCGGGACAGTGTTCATCTTCCGTGCTCACTGTG 2055  
Qy 690 IAG1UHI1SANSERARGARGPHEARG1YARGH1STRYSTRPLYS1PROYR1THGLIN 710  
Db 2056 CCGAGACACACAGCAGATTCAGAGGGCGGACATRCACAGTGAAGCTTTACACTCAAG 2115  
Qy 710 A1GLUAPRGLNAPLEUCYSLYLEUTYR1CYA11EAG1UGLYPHEAPHPHEPHES 730  
Db 2116 TAGAAGATAGGACTTATGCAAACTCTACTGTA1CCCAAGAGATTTGATTTCTCTTT 2175  
Qy 730 ERLEUSERANLYSVALYSAENGLYTHR1PROCYSESERGLUBSPERARGANVALCYE1 750  
Db 2176 CTTTGTCAATTAAGTCAAAAGTGGACTCCAGTCCGAGAGATAGCCGTAAATGTTTGA 2235  
Qy 750 IASAPGLY11EYSCYGLUARGVALGLYCYASPASANVAL1EUGLYSERAP1AVALGLUA 770  
Db 2236 TAGATGGGATATGTGAGAGATTTGATGACATCTCTTGATGTGATGCTGTTGAAG 2295  
Qy 770 BPVALCYSG1YVALCYSAENGLYSAENASER1ALCYSETHR11EH1SARG1YLEUTY 790  
Db 2296 ACGTCTGTGGGTGTGTAA1CGGGAATTA1CTCAGCCGTCACAGATTCA1CAGGGGTCTCTACA 2355  
Qy 790 HTLYH1SH1SH1STRASNG1N1TYR1H1METAL1H1LEPROSERGLYAL1AARG 810  
Db 2356 CCAAGACACACACACACAGATTAATCACATGTGTCCAA1TCTTTGAGAGCCCGGA 2415  
Qy 810 ER11EARG11EYR1G1UWETASNAVALSER1THSER1YR11ESERVALARGANALALEUA 830  
Db 2416 GATTCGCATCTATGAATGAAGCTCTCTACCTCTCA1TTTCTGTGCGCAATGCCCCCTCA 2475

Qy 830 IARGTYR1YR1EUAENGLYH1STR1PR1H1VALASP1TR1PROGLYARGTYR1YSPHESERG 850  
Db 2476 GAAGGTACTACTGATGGGCACTGACCGTGGACTGGCCCGCGGTCAATTTTCGG 2535  
Qy 850 IYTHTR1PHEASPYR1YARGASER1YR1ANG1NPROGLUBANLEUL1EAL1ATN1RGLY 870  
Db 2536 GCAC1ACTTTCAC1YRACAGACGCTCTATTAATGACCCGAGAACTTAATCGCTACTGAGAC 2595  
Qy 870 ROTHRASNG1UTHR1EUL1EVAL1GLUL1EUPHEGL1NG1YARGANPROGLYVAL1A1AT 890  
Db 2596 CAACCAAGACACATGATTTGAGAGTGTCTGTTCAAGGAAGAAACCGGTGTTGCT 2655  
Qy 890 IYGLUTYR1SERWETPRO1ARGLEUGLYTHR1GLULYEG1NPROB1A1AG1NPROSETR1Y 910  
Db 2656 GGGAA1TACTCCATGCTGCTGCTGGGACCGAGAAACAGCCCTGCGCCAGCACTACA 2715  
Qy 910 HTTR1A11EVAL1ARGSERGLUCYSESERVALSERCYSG1YGLYGLYARG 926  
Db 2716 CTTGGCCATCGTGCCTGTGAGTCTCCTGTGCTGCGGAGGGGACXG 2765  
RESULT 11  
US-09-981-151A-5  
Sequence 5, Application US/09981151A  
Publication No. US20030212256A1  
GENERAL INFORMATION:  
APPLICANT: Edinger, Shlomit R  
APPLICANT: Gerlach, Valerie  
APPLICANT: MacDougall, John R  
APPLICANT: Malvankar, Muriel M  
APPLICANT: Smithson, Glenda  
APPLICANT: Millet, Isabelle  
APPLICANT: Peyman, John A  
APPLICANT: Stone, David J  
APPLICANT: Gunther, Erik  
APPLICANT: Ellerman, Karen  
APPLICANT: Shinkels, Richard A  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Guo, Xiaojia  
APPLICANT: Patrujan, Meera  
APPLICANT: Taupier Jr, Raymond J  
APPLICANT: Burgess, Catherine E  
APPLICANT: Zernusen, Bryan D  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Spytek, Kimberly A  
APPLICANT: Gangolli, Esma A  
APPLICANT: Fernandes, Elma R  
APPLICANT: Gorman, Linda  
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-168  
CURRENT APPLICATION NUMBER: US/09/981,151A  
PRIOR FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 60/241,040  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,058  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,063  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,243  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/242,152  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/242,482  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,611  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,612  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,880  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/242,881  
PRIOR FILING DATE: 2000-10-24  
Remaining Prior Application data removed - See File Wrapper or PALM.

```

; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2902
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-981-151A-5

Alignment Scores:
Pred. No.: 0 Length: 2902
Score: 3720.00 Matches: 739
Percent Similarity: 73.67% Conservative: 25
Best Local Similarity: 71.26% Mismatches: 59
Query Match: 71.05% Indels: 216
DB: Gaps: 16

US-09-981-151D-8 (1-952) x US-09-981-151A-5 (1-2902)

QY 11 LeuAlaAlaLeuTrpMetLeuLeuAlaGlnValaGlnValaSerProGlyArgSer 30
DB 1 TTGGCGGCGCTGTGATGCTGCTGCCAGGTGGCGAGGAGTGAATCCCGGGCGCTCC 60
QY 31 HisGlnArgGlyAsnArgGlySerGlyGlnLeuGlnAlaSerProProAlaGlyLeuSer 50
DB 61 CACCAAGGCGGAAACCCGGGCTCGGACAGCTGAGGCGAGTCCCGCGGCTCTCTCC 120
QY 51 ArgGlyProArgArgLeuThrAlaMetSerProLeuPheSerAlaGlyThrCysValArg 70
DB 121 GGGGAGCCCGCGCTCCACCGCGATGCGCGCTGTTTCCGAGGACACCTGGCGC 180
QY 71 HisGlyThrArgSerGlySerAlaTrpGlnProGlnArgProAlaSerSer-SerThrArg 90
DB 181 CATGGGACCCGCGAGCGGCGAGGCTGGAGCCGAGGCTCCCGGCTCTCTCCA----- 235
QY 90 GgLyAlaAlaGlyLeuAspGlyLyGlyArgAspMetAspGlyAlaGlyAsnHisArgSe 110
DB 235 ----- 235
QY 110 rGlnGlnThrAsnThrGlyThrGlnuAsnGlnThrLeuHisValLeuThrGlnTrpAspLe 130
DB 236 -----GACCT 240
QY 130 uValSerAlaTrpGlyuValAspHisArgGlyAspTrpValSerHisGlyuIleMetHisHis 150
DB 241 GGTCTCGCTTACGAGGTTGACACAGGGCGAGTTAGTGTCCCATGAATATCATGACCA 300
QY 150 GglnArgArgArgAlaValAlaValSerGlyuValGlnSerLeuHisValLeuArgLeuLy 170
DB 301 TCAAGCGCGGAGAAAGACAGTGGCGCTGTCGAGGTTGAGCCAGCTTCTCCAGGTATG 360
QY 170 GgLyProArgHisAspPheHisMetAspLeuArgThrSerSerSerLeuValAla----- 188
DB 361 CAGAGCCAGG-----GAGCTCAGACTGTGTGTGAGGCTTTTCCCATGTCTAATTC 411
QY 189 -----ProGlyPheIle----- 192
DB 412 TCAGCGGGGTTTTTGAACCTTCCCATGTTCCGCTCAGTGGAGGGAACAGATGTTCC 471
QY 193 -----ValGlnThrLeuGlyLyThrGlyThrLySerValGlnThrLeuProProGly 210
DB 472 CAAAGAAATATTAACAAATCAATGCTTGGAGAAATCGGCTTGCTTCCATCCAGAAAGTC 531
QY 210 uAsp-----PheCysPheTrpGln-----GlySerLeuArgSerHis-- 222
DB 532 TAAATGTGTTTTCTTTCTTTCTTTATTTTTCACAGTCAAGGACGTGATACAGAAAGA 591
QY 223 -----ArgAsnSerProSerHis-----GlyGlyLySerPheCys 233
DB 592 GGCAGATTACTTCTTAAGGCACTTCTTCAACACCTTCATGAGAAACTGGCAGAGAGTCG 651
QY 233 GgLyGlySer-----GlyGlyLySer-----ThrArgTrn 239
DB 652 CCAAGGACGCTCGCATCCACAGTACTGTACAAGAGAGAGAGCTCTGTGACTCAAGAGAC 711
```

```

QY 239 rLeuLyLeuCysAsnSerGlnLySerCysProArgAspSerValAspPheArgAlaAlaGly 259
DB 712 ATGGAGACCTGGACATCA-----CCCTCGACACAGAGGACCTTGGCTGGGACT 762
QY 259 nCysValaGlnHisAsnSerArgArgPheArgGlyArgHisGlyTrpLySerTrpLyProGlyTrn 279
DB 763 G-----CCAAAGACAGCATTTCTGTGGAAAGCCCAAGAAA----- 799
QY 279 rGlnValGlnAlaAspLeuCysLySerTrpCysIleAlaGlnGlyPheAspPhePheHis 299
DB 799 ----- 799
QY 299 eSerLeuSerAsnLyValLyAspGlyThrProCysSerGluAspSerArgAsnValCys 319
DB 799 ----- 799
QY 319 vIleAspGlyIleCysGlnLeuSerValAlaSerThrSerAlaHisMetProGlnProTr 339
DB 800 -----TACATGCCCGGCTCC 816
QY 339 GLyGlyuAspLeuPheIleLeuProAspGlyuTrpLySerCysLeuArgHisGlyAspArgSe 359
DB 817 CAAAGAAAGACCTTCACTTGCAGATGAGTAAAGTCTTGCTTACGGCATAAAGGCTC 876
QY 359 rLeuLeuArgSerHisArgAsnGlnGlyLeuAsnValGlnThrLeuValAlaAspLy 379
DB 877 TCTTTCAGAGTCCCATAGAAATGAAGACTGAACGTGGAGACCTTGGTGGTGCAGAA 936
QY 379 GLyMetMetGlnAsnHisGlyHisGlyuAsnIleThrTrpValLeuThrIleLeuAs 399
DB 937 AAAGATGATGCAAAACCATGGCCATGAAATATCACCACTGATGTCGATGATCTCA 996
QY 399 nMetValSerAlaLeuPheLyAsp----- 407
DB 997 CATGATATCTGCTTATTCAAAAGATGAACAAATAGAGAAACATCAACATTGCAATTGT 1056
QY 407 ----- 407
DB 1057 AGGTCTGATTTCTTGAAGATGAACAGCCAGACTGTGATGAATAGTACACACGACAGCA 1116
QY 408 -----GlyLeuMetGlyLyAspGlyThrArgHis 417
DB 1117 CACCTTAAGATGTTTTCGCAAGTGCAGTCTGTGATGATGGGAAAGATGGAGCTGTCA 1176
QY 417 sAspHisAlaIleLeuLeuThrGlyLeuAspIleCysSerTrpLyAsnGlnProCysAs 437
DB 1177 TGAACACGCGCATTTACTGACTGTGTGATATATGTCTCTGGAAAGATGAGCCGTGTA 1236
QY 437 rThrLeuGlyPheAlaProIleSerGlyMetCysSerLySerTrpArgSerCysThrIleAs 457
DB 1237 CACTTGGGATTTTGACCCCATAGTGAATGTATGATTAATATCGACGTGCAGCATTA 1296
QY 457 nGluAspTrnGlyLeuGlyLeuAlaPheThrIleAlaHisGlySerGlyHisAsnPheGly 477
DB 1297 TGAAGATACAGGCTTGAGCTTGACCTTCAACATTTGCCATAGTCCGACACAACTTTGG 1356
QY 477 yMetIleHisAspGlyGlnGlyuAsnMetCysLySerLySerGlnGlyuAsnIleMetSerPr 497
DB 1357 CATGATTTCAAGAGGAGAAAGGAAACATGTGCAAAAGATCCGAGGGAACATTCATGCC 1416
QY 497 oThrLeuAlaGlyArgAsnGlyValaPheSerTrpSerProCysSerArgGlnTrpLeuHis 517
DB 1417 TACATTGGCAGAGCGAATGAGAGTCTTCTCTGTGTACCTCTGACGCGCCAGATATACA 1476
QY 517 sLySerPheLeuSerThrAlaGlnAlaIleCysLeuAlaAspGlnProLyProValLyGly 537
DB 1477 CAATTTCTTAAGACCGCTCAAGCTATCTGCTGTGATACGCAAAAGCTGTGAAGGA 1536
QY 537 uTrpLySerTrpProGlnLyLeuProGlyuLeuTrpAspAlaAsnThrGlnCysLySerTr 557
DB 1537 ATACAAGATATCTCGAAGAAATTCGACAGAGAAATTAATATGTGTGCAAAACACAGTGAAGTG 1596
```



```
QY 557 pginhegllygllybalaalyetucywmelleuapbhegllybalaaprllecyalyal 577
DB 1597 GCGATTGCGAGAGAAAGCCAGAGCTGCAATGCTGCACTTTAAAGACATTCGTAAAC 1656
QY 577 aleutrcywhiarglleglyarglyscylutrllyrphemetproalalaglul 597
DB 1657 CCTGTGTGTCATCGTATGGAAGAAATGTGAGACTAAATTTATGCGACAGACAAAG 1716
QY 597 ythrllecygllyhiapbmettrpcyarggllygllycysvallyetlyyapgl 617
DB 1717 CACAAATTTGGGCGATGAACA-TGGTGCC--GGAGAGACAGTGTGTGAATATGTGATGA 1773
QY 617 ucllyrplyrprocthihgllyhiatrpseraprtprsetsertrpcyasertr 637
DB 1774 AGGCCCCAAGCCCAACCATGCGACATGCGATGCGATGCTCTTGTGTCCCAAGCTCCAG 1833
QY 637 gtrhrcygllygllyvalserhiargserarg--leucyethasnpblyrprose 656
DB 1834 GACCTCGGAGGGGAGATCTCATAGAGTCCCTCAAAATKACATTCAGGCGCATC 1893
QY 656 rhiagllylyrphercyagllysertharqthrlleuylcyasanserlly 676
DB 1894 GATGAGAGGAAGTTCTGTGAGGGCTCCACTGCGCACTGAGCTCTGCAACAGTCAGAA 1953
QY 676 scyrcpoadgarpservalasrphearghalalaglncllyahlnhiasnerargr 696
DB 1954 ATGTCCCGGAGACAGTGTGACTTCGTGTCTGTCTGATGCGGACACAAACGACGAGC 2013
QY 696 gpheargllyarghietylyetrllyrplyrprolyrthrglnvalgluapglapblycy 716
DB 2014 ATTCAAGGGCGGCACTACAGTGAAGCT-----GATCAGAGCTTANG 2058
QY 716 elylyeutyrcyallagllygllyrphearpberpberseuaserasnllyvally 736
DB 2059 CAAACTCTGATGAGCAGAAAGATTTGATTTCTTTCTTTCTTCAATTAAGTCA 2118
QY 736 baprglythrrpcyasergllybapserarganvalcyellleapgllylecyegllyr 756
DB 2119 AGATGGAGCTCCATGCTCGAGAGATAGCCGTAAATGTTGTATAGAGGATATGAGAG 2178
QY 756 gvalgllycyasarpasvalleuglyserasrpalalalgluapvalcyagllyvalcyas 776
DB 2179 AGTTGATGTGACAAATGCTCTTGATCTGATGCTGTGAAGAGCTGTGGGGTGTGTA 2238
QY 776 ncllyanbanaseralacysethrllehiarggllyeutylyrthlywhishisthas 796
DB 2239 CCGGATATACCTAGCCTGACAGTTCACAGGGGTCTCTACCTA----- 2281
QY 796 nglnlyrlyrhiamevalthrleprosergllyalargserllearglletyrqlume 816
DB 2282 -GAGTATTAACAATGTGACCAATTCCTTGTGAGCCCGGAGATTCGCACTATGAAT 2340
QY 816 casnvalserthsertrileservalarganlalaleuargarglytyrleuansgl 836
DB 2341 GAACGCTTACTCTTACTATTTCTGTGGCAATGCCCTCAGAGGATCTACTGAATGG 2400
QY 836 yhiatrpthrvalasrtrpccgllyargtyrlyrphesergllyrth-rphasrlyrtr 856
DB 2401 GCACTGAGCCGTGACTGCGCCGCGGTACAAATTTTGGGCACTACTTGCATACAG 2460
QY 856 garserlyraangluProglubansleuilealathrglyrprothraangluThrlleu 876
DB 2461 AGCGTCTTAATAGACCCGAGAACTTAATCGTACTGAGCAACCAAGAGACACTGAT 2520
QY 876 evalgluleuleupheglnglyarganpccgllyvalalatrpgllyrsemeProxr 896
DB 2521 TGTGGAGCTGCTGTTTCAAGGAAAGAACCCGGGTGTGTGCTGGAAATATCTCATGCTCG 2580
QY 896 gleuglythrglylygllyrproproalaglnproserlyrthrrpalalilevalargse 916
DB 2581 CTGGGAGACCGAGAGCAGCCCTGCGCCAGCCAGCTACACTGGGCGCATGTGCGCTC 2640
QY 916 rcllycyaserValsercyegllygllyargcybseuprovalleuleuleuglualal 936
```

```
DB 2641 TTAGTGTCCGTGCTCTGCGAGGGAGTGGTGCCTTCCAGTGTGCTTGGAGGAC 2700
QY 936 aCysglpProserAlatrhalatyrilalaleuAlapheleuglusser 952
DB 2701 ATGTACGCTTTAGCCATCGCGCTACATTCGACTGCGCTTTCTTGAATCC 2749
```

## RESULT 12

US-10-399-645-19

Sequence 19, Application US/10399645

Publication No. US20040029249A1

## GENERAL INFORMATION:

APPLICANT: INCYTE CORPORATION; LEE, Ernestine A.

APPLICANT: HARALIA, April J.A.; YUE, Henry

APPLICANT: LAU, Preeti G.; YAO, Monique G.

APPLICANT: LU, Yan; CHAWLA, Nandinder K.

APPLICANT: WARREN, Bridget A.; LU, Dying Aina M.

APPLICANT: BAUGHN, Mariah R.; DELGEBANE, Angelo M.

APPLICANT: BURFORD, Neil; BOROMSKY, Mark L.

APPLICANT: LEE, Sally; XU, Yuming

APPLICANT: GRIFFIN, Jennifer A.; KALLICK, Deborah A.

APPLICANT: GANDHI, Ameena R.; ARVIZU, Chandra S.

APPLICANT: ISON, Craig H.; TANG, Y. Tom

APPLICANT: AZIMZAI, Yalda; ELLIOTT, Vicki S.

APPLICANT: SMARNAKAR, Anita; RAMKUMAR, Jayalaxmi

APPLICANT: NGUYEN, Damien B.; TRIBOULEY, Catherine M.

APPLICANT: LO, Terence P.; AU-YOUNG, Janice K.

APPLICANT: THANGAVELU, Kavitha; KEARNEY, Liam

TITLE OF INVENTION: PROTEASES

FILE REFERENCE: PI-0263 USN

CURRENT APPLICATION NUMBER: US/10/399,645

CURRENT FILING DATE: 2003-04-16

PRIOR APPLICATION NUMBER: PCT/US01/51034

PRIOR FILING DATE: 2001-10-18

PRIOR APPLICATION NUMBER: US 60/241,573

PRIOR FILING DATE: 2000-10-18

PRIOR APPLICATION NUMBER: US 60/243,643

PRIOR FILING DATE: 2000-10-25

PRIOR APPLICATION NUMBER: US 60/245,256

PRIOR FILING DATE: 2000-11-02

PRIOR APPLICATION NUMBER: US 60/248,395

PRIOR FILING DATE: 2000-11-13

PRIOR APPLICATION NUMBER: US 60/249,826

PRIOR FILING DATE: 2000-11-16

PRIOR APPLICATION NUMBER: US 60/252,303

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,981

PRIOR FILING DATE: 2000-12-01

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PERL Program

SEQ ID NO 19

LENGTH: 4888

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc.feature

OTHER INFORMATION: Incyte ID No. US20040029249A1 3533147CB1

US-10-399-645-19

## Alignment Scores:

Pred. No.:	0	Length:	4888
Score:	3291.50	Matches:	624
Percent Similarity:	78.61%	Conservative:	19
Best Local Similarity:	76.28%	Mismatches:	63
Query Match:	62.66%	Indels:	112
DB:	17	Gaps:	10

US-09-981-151D-8 (1-952) x US-10-399-645-19 (1-4888)

```
QY 211 AspPheCySpheTYrGlnGlySerleuArgSerHisArganser----- 225
DB 285 GAATTCGCACTTAATTTGTGGACATTAACAGCAATATGTTCCAAACAGCATTAATTCATTAA 344
```



QY	226	-----ProserHisglgylgyluyspHeCys-GluGluyserThrArgThrleu	241
		:::	
Db	345	ntgGCGCAAGCCAAAAATGCTCGTGGAGATTAAACAGAAAGTGACTTCAGGGAGCTTCG	404
QY	241	leuCYsaansersglnlyCys-----ProArgaspserVa	253
Db	405	T---GGTAACACCCACCACTGCCCTGACCAAAAAGGCTTAGAAATGCTCTCCAGGCTT	461
QY	241	laephEarlaalaInCys-----AlaGlunHsaensersArgArpHeArgslYAr	271
		:::          :::          :::          :::	
Db	462	GCAgTTCACTACGTCAAAATGTCGTGACATCAGACAGCCACCCATCAGGGCT	521
QY	271	gHisrYrlysrTrpYsProYrThrGlnValGluHlaeArpLeuCYslyleuYrCYsll	291
Db	522	TCACATAC-----GTGACATTAAATTCAGCAGCATGATAGC	554
QY	291	eAlaGlulglYpHeaArpPhe-----PheSerleuSe	302
Db	555	AACAGAAAGGCGACGATTACTCTCTTAAGGCCACTTCTTACACCTTCATGGAATCTGG	614
QY	302	rAenlysaVallysaerGlYThrProCYsSer-----GluaspSerArghsnValCY	319
		:::          :::          :::          :::	
Db	615	CAGAGCTGCCCAAGGAGCTCGGCATCCACGATCTGTAAGATGATCCACAGAGCCCA	674
QY	319	eIlleaprglYleCYsGluLeuSerValYalsersrSer-----AlaHis-----	334
Db	675	TGCTCCTGGGGCAGTGAAGCTCTGTGTGACTCAAGACATGGGAGCTGGACATCAACC	734
QY	334	-----	334
Db	735	CCTGCACAGCAGCAGCTTCGCGCTGGGACTGCCCAAAAGCAGCATTTCTGGAAAGACG	794
QY	335	-----MetProGlnProProlysglunAspleuPheleleuProaspGlunYrly	351
Db	795	CAAGAAATACATGAGCCCGACGCTCCCAAGGAAGACCTCTTCACTTGGCAGATGATATA	854
QY	351	sSerCYsleuArghHslysaYserserleuLeuArgrsErHsaYsGluGlulLeuAsnVa	371
Db	855	GTCTTGCTTACCGGCATTAAGCGCTCTCTTGTGAGGTCCCATGAAGAAATGAAATCGA	914
QY	371	lGluThrleuValValAspLylyMetMetGlnasnHlsglYHlGluAsnLlePh	391
Db	915	GGAGAGCTTGAGTGGTGGTGCACAAAAGATGATGCAAAACATGGCCATGAAGAAATATCAC	974
QY	391	rThrYrValleuThrHlleuAsnMetValserAlaleuPheLYasp-----	407
Db	975	CACCTACGCTCTCAGATACTCAACATGSTATCTGCTTATTTCANAGATGAACAATAAG	1033
QY	407	-----	407
Db	1035	AGGAACATCAACATTGCAAATTGTAGGTCTGATCTTCTTAGAAGATGAACAGCAGAGCT	1099
QY	408	-----Glyle	409
Db	1095	GGTGATTAAGTCAACAGCAGACACACCTTAAGTAGCTTCTGCAGCTGCAGCTGGAGTT	1155
QY	409	uMetGlYlysaerGlYThrArgHlAspHlIsaHlleleuLeuThrGlYleuAspLleCY	429
Db	1155	GATGGGGAAGATGGGACCTCGTCATGACCAAGCCCATCTTACTGACTGGTGTGGATTAAG	121
QY	429	sSerTrpYsaenGluProCYsaSPThrleuGlYpHeaLaprolIseserGlYmetCYsse	449
Db	1215	TTCTCGGAAGATTAAGCCCTGTGACACTTCTGGGATTTGGACCCATTAAGTGAATGTGAG	127
QY	449	rlysrYrArgrsErCYrThrHleasnGluAspHrgrlYleuGlYleuAlaPheThrHleAl	469
Db	1275	TAAATATGCGACCTGCACATTAATGAATACAGGCTCTTGACCTGGCCTTACCACTTGC	1333
QY	469	aHlsgluserGlYHlAsnPhGeGlYmetLleHlAspGrlyGlulYAsnMetCYslyslY	489
Db	1335	CCATAGTCTGGAACACAACTTTGGCATGATTCATGATGAGAAAGGAACATGTGTAAAAA	1399
QY	489	sSerGlulglYasnLleMetSerProThrleuHlaGlYArGaenGlYValPheSerTrpSe	509

Db	1395	GTCCGAGGGCAATCATGTCCTTACATTGGCAGGCGAATGGAATCTTCTCTGTC	1454
Qy	509	rProCySeSerArgGlnTyrlrEuhiSlvsPheLeuSerThrAlaGlnAlaIleCySeLeuAl	529
Db	1455	ACCTTGACGGCGCAGATATCTACACAAATTTCTTAAGACCGCTCAAGCTATCTGCGCTTGC	1514
Qy	529	aAspGlnProLybProVallysgLutTyrlsTyPProGluLysLeuProGlygluLeuTy	549
Db	1515	TGATCACCACAAAGCGCTTGAAAGGAATCAAGTATCTCGAAGAAATTCGCAGAGCAATATTA	1574
Qy	549	rAspAlaAsnThrGlnCyglvslrPrpGlnPheGlygluLysAlaLysLeuCySeMetLeuAs	569
Db	1575	TGAAGCAAAACACACAGTGAAGTGGCGATTCGAGAGAAAGCCAAAGCTTCGCATGCTGGA	1634
Qy	569	pPheLysLysAspIrlleCySlyslsAlaLeuTrpCyShIleGlyrgrlvsCySgluTh	589
Db	1635	CTTTAAAABAAGACATCTGTAAAGCCCTGTGTGTCCTCATGTTGGAAAGAAATGTAGAC	1694
Qy	589	rLysPheMetProAlaAlaGluGlyThrIleCySglYhiAspMetTrpCySarglYgl	609
Db	1695	TAAATTTATGCGACGACAGACAGAAAGGCAAAATTGTGGGCATGACATGTGTGCGGGAGG	1754
Qy	609	yGlnCyVallyslTyrglyAspGluGlyLProLybProThhiSGlyhiStrPserAspTr	629
Db	1755	ACAGTGTGTAAATATGTGTATGAAAGGCCCAAGCCCAACCATGCGCACATGTCGACTG	1814
Qy	629	pSerSerTrpSerProCySerArgrThrCySglYglYglYValSerhiSarPserArgLe	649
Db	1815	GTCTTCTTGGTCCCCATGCTCCAGAGCTTCGGAGGGGGAGTATCTCATAGAGTCGGCTT	1874
Qy	649	uCyStrAsnProLybProSerhiSGlyglYlvsPheCySgluGlyserThrArgrThle	669
Db	1875	CTGCACCAACCCCAAGGCATCGCATGGAGGGAAGTTCTGTGAAGGCTCCACTCGCACTCT	1934
Qy	669	uLysLeuCyAsnSerGlnlyscYsProlaGAspSerValAspPheArgAlaIleGlnCy	689
Db	1935	GAAGCTCTGCAACAGTCAGAAATGTCGCCGGAGCAGTGTGACTTCGTCCTCGTCACTG	1994
Qy	689	sAlaGlnhiASnSerTrgrArgrPheArgrGlyAArghiSTyrlvsTrpLysProTyTrThrl	709
Db	1995	TGCCGAGCAACAACGACGATGATTCAGAGGGCGGCACTCAAGTGGAAAGCTTACACTCA	2054
Qy	709	nValGluAspGlnAspLeuCySlyslsLeuTyrcYsIleAlaGluGlyPheAspPhePheP	729
Db	2055	AGTAGAAGAGTACAGGACTTATGCAAACTCTATCTGATGCGAAGAGATTGATTTCTTCTT	2114
Qy	729	eSerLeuSerAsnLysVallyAspGlyThrProCySserGluAspSerArgAsnValCy	749
Db	2115	TTCTTTGTCAAAATAAAGTCAAAATGAGGACTCCATGCTCGAGAGATAGCCGTAAATGTTTG	2174
Qy	749	sIleAspGlyIleCysGluArgrValGlyCySAspAsnValLeuGlySerAspAlaValG	769
Db	2175	TATAGATGGGATATGTAGAGAGTGGATGTGCAATGTCTTGAGATCTATGCTGTGTA	2234
Qy	769	uAspValCySglYValCySAsnGlyAsnAsnSerAlaCyStrIleGhiSarGlyLeuTy	789
Db	2235	AGACGTCTGTGGGGTGTGTAAACGGAAATACTAGCTGTGACGATTCACAGGGGCTCTTA	2294
Qy	789	rThrLysHiGhiGhiStrhAsnGlnTyTrhIsmetValThrlleProSerGlyAlaAr	809
Db	2295	CACCAAGCACACACACACCAACAGATATATCAACATGTACACACTTCTTCTGAGGCCG	2354
Qy	809	gSerIleArgIleTyrgluMetAsnValSerThrSerTyrlleSerValArgAsnAlaLe	829
Db	2355	GAGATCTCGCATATAGAAATGAAACGCTCTTACTCTCTTAATTTCTGTGGCAATGCCCT	2414
Qy	829	uArgArgTyTrylvsAsnGlyhiStrPThrValAspTrpProGlyAArgTyrlvsPheSe	849
Db	2415	CAGAAGTATTACTGATGGGCACTGGACCGTGGACTGGCCCGCCGGTACAAATTTTTC	2474
Qy	849	rGlyThrThrPheAspTyTrArgArgSerTyraAsnGluProGluAsnLeuIleAlaThrG	869

Db 2475 GGGCACTACTTTCGACTACAGACGGTCTTAATGAGCCCGAGAACTTAATCGCTACTGG 2534  
QY 869 YPOTHRAENGJLTHLEULEVAlGJLULEUPHENGJLYARGASPROGJLYVALI 889  
Db 2535 ACCAACCAAGAGACACTGATTTGTGAGCTGTGTTTACAGGAGAACCCCGGTGTTCG 2594  
QY 889 ATTPGJLTYRSEMERPROARGLEUJLYTHRGJLYLVBGINPROALAGLNPROSEPTY 909  
Db 2595 CTGGGAATACCTCATCTCGCTTGGGAGACCGAAGACAGCCCTGCCCCAGCCAGCTTA 2654  
QY 909 TTHTRPALAILLEVALARGSERGLUCYSERVALSERCYSGJLYGJLYARG 926  
Db 2655 CACTTGGGCATCTGTCGCTCTGAGTGCTCCGTCTCTGGAGGGGGAGACAG 2706  
RESULT 13  
US-10-363-937-34  
Sequence 34, Application US/10363937  
Publication No. US20040053269A1  
GENERAL INFORMATION:  
APPLICANT: Todd, Stephen; Delegeane, Angelo M.;  
APPLICANT: Gandhi, Ameena R.; Nguyen, Daniel B.;  
APPLICANT: Hafalia, April J.A.; Kearney, Liam;  
APPLICANT: Lu, Yan; Lee, Ernestine A.;  
APPLICANT: Chawla, Narinder K.; Das, Debopriya;  
APPLICANT: Arvizu, Chandra S.; Yao, Montique G.;  
APPLICANT: Kallick, Deborah A.; Elliott, Vicki S.;  
APPLICANT: Ding, Li; Yue, Henry;  
APPLICANT: Reddy, Roopa; Butford, Neil;  
APPLICANT: Baughn, Mariah R.; Lal, Preeti G.;  
APPLICANT: Borowsky, Mark L.; Lu, Dyrung Anna M.;  
APPLICANT: Runkumar, Jayalaxmi; Yang, Junning;  
APPLICANT: Tribouley, Catherine M.; Khan, Farrah A.;  
APPLICANT: Gurturajan, Rajagopal; Tang, Y. Tom;  
APPLICANT: Au-Young, Janice; Warren, Bridget A.;  
APPLICANT: Hernandez, Roberto; Dugan, Brendan M.  
TITLE OF INVENTION: PROTEASES  
FILE REFERENCE: PI-0212 USN  
CURRENT APPLICATION NUMBER: US/10/363,937  
CURRENT FILING DATE: 2003-03-04  
PRIOR APPLICATION NUMBER: PCT/US01/28161  
PRIOR FILING DATE: 2001-09-06  
PRIOR APPLICATION NUMBER: US 60/231,039  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: US 60/232,812  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: US 60/234,850  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: US 60/236,500  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: US 60/238,773  
PRIOR FILING DATE: 2000-10-05  
PRIOR APPLICATION NUMBER: US 60/239,658  
PRIOR FILING DATE: 2000-10-11  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PERL Program  
SEQ ID NO 34  
LENGTH: 3389  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. US20040053269A1 7478405CBI  
US-10-363-937-34  
Alignment Scores:  
Pred. No.: 7,12e-243 Length: 3389  
Score: 2442.00 Matches: 486  
Percent Similarity: 63.468 Conservative: 127  
Best Local Similarity: 50.318 Mismatches: 208  
Query Match: 46.644 Indels: 147  
DB: 18 Gaps: 22  
US-09-981-151d-8 (1-952) \* US-10-363-937-34 (1-3389)

QY 46 PROARGLEULESERARGJLYPROARGJLEUTHRALEMERSEPROLEUPHESERALA 65  
Db 42 CGCGCTTGCCACCGGAGCGCGCGGTCCGACCTGACCA-----TGAGTGG 92  
QY 66 GJLYTHRCY-----ValArgHISGLYThr---Arg 74  
Db 93 CCTCTGCTCGCGTGCCTTCCGGCTCGGGTTGGGCCCCCGGAGGGGCTGGCGG 152  
QY 75 SERGLYSERLATRP-----GluPro 81  
Db 153 GACGTGGGGGCGTGGCCAAAGCGCTCCAGCTGTGCTGCTGCTGTGCTGCTGCGG 212  
QY 82 GJLYARGPROALASERSETHARGJLYALAGJLYLEUAPGLYVGLYARGAP 101  
Db 213 CGGCGCTTA-GCCAGTGAAGAGCAGCGCGCGCGGACGATTAAT----- 256  
QY 102 METAPRGJLYALAGJLYASHISARGSERGLNTHRAENTHGLYTHRGJLYASNGJLTHR 121  
Db 256 ----- 256  
QY 122 LEUHISeValLeuThrgJLThrgArLeuValSerAlaTYGJLYVALASPHISARGJLYAP 141  
Db 257 -----GATGATTAAGCTCTTTGTACGCGCAGTGAAGATGACTCCAGCGGTCA 304  
QY 142 TYRVALSERHISGLJLYEMECHISHSGLNARGARGARGALVALALVALSERGLU 161  
Db 305 TATATTTCACACGACATTTTGCACACGCGGAGAAAGCCGATCG---GCCGAGATGCC 361  
QY 162 VALGJUSERTLEUHISeValLeuThrgJLYVGLYPROARGHISAPRPHISMEKSERLYARG 181  
Db 362 AGAAGCTCCCTGCATCCGATTTTCACGATTTTGACACAGAACTGCACTTAACCTTAAG 421  
QY 182 THRSESERSELEVALALAPROGLYPHEILEVALGJLTHRGJLYSERTHRGJLYTHR 201  
Db 422 ---CCCTGGGCGATTTTGAAGACTCTTTATTTGTCAGGTACTTGGAAGATGCTGT 478  
QY 202 LYSERVALGJLTHRGJLYPROARGJLYASPHISERPHETRYGJLYSERLEUARGSER 221  
Db 479 TCAGAGACTCAGAAA---CCGAGGTGACAGCAATGCTTCATCAGGGAATTCAGAAAT 535  
QY 222 HISARGASERPROSEHISGLJLYASPHISERGLYGLYSERTHARGHIREUYS 241  
Db 536 GAC--AGCTCTCTCTGTGCTGTGTGTACGTGTGCTGTGCTGTGCTGTGCTGTGCT 592  
QY 242 LEUCYASNSERGLN-----LYSCYSPROARGASERVALASPRHEARGLA 257  
Db 593 ACAGCAAAAATGATTCCTCATCTGCCATTACTCAG----- 631  
QY 258 ALAGJLYVALAGJLYHISASNSERARGARGHEARGJLYARGHISLYLYSTRLYSPRO 277  
Db 632 TTCTGGGCCAGAACACAACTACAGCTCCCTGGGGGTCAACAT-----CCT 679  
QY 278 TYRTHRGJLYVALAGJLYALASPRLEUCYVLYSEUITYSVILEAGJLYPHEASR--- 296  
Db 680 CAGTACT-GTACAAAAGAC-----AGCAGAGAGAAAGATCA 717  
QY 297 -----PhePheSerLeuSerAanLYVal---LYSAPGLY 308  
Db 718 GCGGTACCGGTGCTACCCCGGTGCGCGGATTTATCTGTTACTCCCAAGTCACAT 777  
QY 309 THRGJLYSERGLYASPRSERARGAN--VALCYVILEASPRJLYLYCYGJLYLEUSER 327  
Db 778 TCCCATCATCTCAGAGTGCAGAGACAGAGTATCACCATCGAAGGTGCAAAACAGACA 837  
QY 328 VALVAL---SERTHR-SERALHISMERPROGLYPROARGJLYASPRLEUPHEILELE 346  
Db 838 TTTTGTGAGAGAGCAAGAAATATGCTCCCAAGGCTCCCAAGAGACACTTACTAAG 897  
QY 346 UPROARGJLYTYRLYSERSEYVLEUARGHISLYHARGSERLEUASERHISARGAV 366  
Db 898 GTTTGATGATATGGAGCTCTGGGCGACCAAGAGATCACTGGAAATATCAAAAGGG 957

OY		366	nGLUlnIuleuhenVlGIuThrleuValValValaerlyuylseMetcGlnaenhiGI	386
Dd		958	C-----TCAATGTGGAAACCCCTGTGTGTGCACAAGAAAATGTGTGAAGAAGCATGG	1011
OY		386	yHi eglIuaeniIethrThryrValleuthrIlleuabmetValSerlaaleuPhely	406
Dd		1012	CAAGGAAATGTCAACACATACATTCTCACAGTAATGAACATGGTTTCTGGCCTATTATA	1071
OY		406	sAPRGlY-----	408
Dd		1072	AGATGGACTATTGGAAAGTGACATAAAGTGGTTGGTAGACCTAATTCTTGGAACAA	1131
OY		408	-----	408
Dd		1132	AGAACCTGGAGANTATTGATTCMAACCATCATGACAGACCAATCTCGAATAGTTTTTGCA	1191
OY		409	-----LeumetGlyLyAsPRGlYThrArgHisAPHIsAlailleuLeuth	424
Dd		1192	ATGGCAGCTGCCCTCATTTGGAAAGAAATGGCAAGACATGATCATGGCCATTTTCTAAC	1251
OY		424	rGlyleuapriIeCyserTrpLysasnGluProCyaaPrThrleugilyPhealaProil	444
Dd		1252	AGGATTTGATATTGTCTTGGAAAGATGAACCATGTACACTGAGGTTTGGCCCCAT	1311
OY		444	eSerGlymetCyserSeryrArgSerCythrIlleangluaphThrlgyleuGlyle	464
Dd		1312	CAGTGAATGTGCTCTTAAGTACCAGAAATGTATCCATCATATGAGGACACAGGACTTGCCCT	1371
OY		464	wAlaPherThrIleaiahIasguSeGlyHiasnphelIwetiIehIsAPRGlylgulGI	484
Dd		1372	TGCCTTCAACATCGCTCATAGATCAGGGACACACTTGATGATTCACAGAGGAAGG	1431
OY		484	yASmMeCyalyblvsSerGulGIyASNIIeweserProThrleualagIyArGAsngI	504
Dd		1432	GATTCCTCGCAGAAAGCGTGAAGGCAATATCATGTCTCCACATCGACCGGAACAATGG	1491
OY		504	yValPheSerTrpSerProCyaserArgIntyreuhIylyPheIuseSerThralagl	524
Dd		1492	AGTGTTTTCATGTGTCTTCTGTGACGCGGCAGATCTCAAGAAATTCCTCACACACCTCA	1551
OY		524	nAlalIeCyeteuulaaPRGInProLyProVallyseluTytyrTrpProGluLyble	544
Dd		1552	GCGCGGGGTCTAGTGAATGAGCCCAACAGCAGACAGATTAATTCGCGACAACT	1611
OY		544	uPRoGlyglIeuTyrrARPAIAaenThGInCyalyerTrpGlnPhegiyGluLyvalaLy	564
Dd		1612	ACCAGGACAGATTATGATGCTGTGACACACAGTGTAAATGGCAATTTGGACMAAGCCA	1671
OY		564	sLeuCYawetIeubapPheLyalyAsPRIICyelyaAlaleutPrCyvniIsargIlegI	584
Dd		1672	GTTATGACAGCCTTGGTGTTGTGAAGATATTGGCAATCACTTTGGTGTCCACCGAGTGG	1731
OY		584	yArglybeCyeglIuthrlyvPheMetProAlaalaglulIyhrIlleCyegIyHIsABPM	604
Dd		1732	CCACAGGTGTAGAACCAATTATATGCCCGCAGCAGAAAGGACCGTTGTGTGGCTTGAAGTAT	1791
OY		604	tTrPCyArngIyglInGInCyvaIlyeTrGlyAsPRglulGIProLyserProThrhieGI	624
Dd		1792	GTGGTGTGGCAAGCCACAGTGTAAATTTGGGAGAGCTCGGGCCCCGGCCATTCACAGG	1851
OY		624	yHIsTrpSerApTrpSerSerTrpSerProCyaserXArgThrcyegIyglIyvalise	644
Dd		1852	CSAGNGTCCGCTGTGSAAGTGGTCAAAATGTTCCCGGACATGTGTGGAGGAGTCAA	1911
OY		644	rHIsArgSerArgleuCyethraenPRolyvProsenhi eglIyglIylyvPheCyegIulGI	664
Dd		1912	GTTCCAGAGAGACACTGCAMATMACCCCAAGCCTCAGATGTGTGCATATTCTGTCCAGG	1971
OY		664	ySerThrxArgThrleuLytleuCyvaSnSeGlmLyCySProAdhaPSerValaAPh	684
Dd		1972	TTCNAGCCTATTATCAAGCTGTGCAMAATTAAACCTTGCATATGAATAATAGCTTGGATTT	2031
OY		684	eArgAlaIaGInCyvalaGluHIIsAnSerArgPrheaArgIyArgHIsIyLyvtr	704

Db	2032	TCGGGCTTCACAGGTGTGAGATATTAACAGCAACCTTTCCGTGGATGGTTCTTACAGTGTG	2091
Qy	704	PLySPrcTYrThrgInValGluAerGlnAspLeuCyAlsYleuTYrCYsIlleaIagiIuG1	724
Db	2092	GAAACCCATATCAAAAGTGGAGAGGAAGATGCATGCAACTGTATCTGCAGAACGCTGAGAA	2151
Qy	724	yPhaSPhePhePheSerLeuSerAsnLYsValLYsAspGlyThrProCYsSerGIuAs	744
Db	2152	CTTTGAAATTTTTTTTGGCAATGTCCGGCAAAAGTGAAAGATGGAATCTCCCTGCTCCCAA	2211
Qy	744	pSerArgAsnValCYsIlleaAspGlyIleCYsGluArgValGIYCYsAspAsnValLeuGI	764
Db	2212	CAAAATGATATTGTGATGTACGGGGTTGTGAATCTAGTGGAGATGTATCATGTGAACTAGG	2271
Qy	764	ySerAspAlaValGluAspValCYsGlyValCYsAsnGlyAsnAsnSerAlaCYsThrI1	784
Db	2272	CTCTAAAGCACTTCAGATGCTTGTGGCGTTTGGAAAGGTATATTCACCTTGCAGATT	2331
Qy	784	eHiArgGlyLeuTYrThrLYsHisHisSerHisAsnGlnTYrThrHisMetValThrI1	804
Db	2332	TTATTAAGAGCCCTGTATCTCAACAGCATTAAGCAAAATGAAATATTATCCGGGTGCATCAT	2391
Qy	804	eProSerGIYAlaArgSerIleArgIleTYrGluMetAsnValSerThrSerTYrIleSe	824
Db	2392	TCCAGCTGGCGCCCGAAGCATCGAAATCCAGAGACTCAGAGTTTCTCCAGATTACCTGC	2451
Qy	824	rValArgAsnAlaLeuArgArgTYrTYrLeuAsnGlyHisThrProValAspTrpProGI	844
Db	2452	AGTTTCAGAGCTCAGTCAAAAGTATTACTCTACCCGGGGCTGGAGCATTCAGCTGGCTGG	2511
Qy	844	yArgTYrLYsPheSerGIYThrThrPheAspTYrArgArgSerTYrAsnGluProGIuAs	864
Db	2512	GGAAGTCCCGCTTCGTGGAGACCATGTTGAATAACAGGCGCTTTCAACCGCCCGAAGC	2571
Qy	864	nLeuIleAlaThrGlyProThrAsnGluThrIleValGluLeuLeuPheGlnGlyArg	884
Db	2572	TCTGTACGGCGCAGAGGCGCCCAAAATGAGAGCGCTGTCTTTGAAATTCGTATGCAAGCAA	2631
Qy	884	GAAsProGIYValAlaTrpGluTYrSerMetProArgLeu-----GlyThrGluLYsGI	902
Db	2632	AAATTCAGAGGATGCTTGGAAATGACATTCACCAAGCTCATGAAATGCACT-----	2693
Qy	902	nProProAla-----GlnProSerTYrThrTrpAlaIleValAlaArgSerGIuCYsSerVa	920
Db	2694	-CCACCGAGCCCAAAAGACCTGCTCTATCTCTGAGATCTGTGAGTCAAGTGTCTCGT	2742
Qy	920	LYsCYsGlyCYsGly 925	
Db	2743	CTCCTGTGTGGAGGT 2758	
RESULT 14			
US-10-240-545A-1			
; Sequence 1, Application US/10240545A			
; Publication No. US20030185828A1			
; GENERAL INFORMATION:			
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.			
; TITLE OF INVENTION: No. US20030185828A1el aggreCanase			
; FILE REFERENCE: 08959.0002			
; CURRENT APPLICATION NUMBER: US/10/240.545A			
; PRIOR FILING DATE: 2002-10-02			
; PRIOR APPLICATION NUMBER: PCT/JP01/11033			
; PRIOR FILING DATE: 2001-12-17			
; PRIOR APPLICATION NUMBER: JP 2000-384300			
; PRIOR FILING DATE: 2000-12-18			
; NUMBER OF SEQ ID NOS: 26			
; SEQ ID NO 1			
; LENGTH: 3666			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1)..(3666)			

US-10-240-545A-1

## Alignment Scores:

Pred. No.:	7,99e-243	Length:	3666
Score:	2442.00	Matches:	483
Percent Similarity:	63.58%	Conservative:	128
Best Local Similarity:	50.26%	Mismatches:	211
Query Match:	46.64%	Indels:	141
	16	Gaps:	20

US-09-981-151d-8 (1-952) x US-10-240-545A-1 (1-3666)

```
QY 27 ProGlyAArgSerHieGlnAArgGlySerGlyGlnLeuGlnAAspProPro 46
Db 29 CCTCCCGGCTGGCGGGTTCCGGCCCGCCGAGGGGCTGGGGCGGTGGCCCA 88
QY 47 ArgLeuLeuSerArgGlyProArgArgLeuThrAlaMetSerProLeuPheSerAlaGly 66
Db 89 AGGCGCTCCGAC-----TGTGCTGCC 109
QY 67 ThrCysValArgHieGlnThrArgSerGlySerAlaTPrGluProGluArgProAlaSer 86
Db 110 TCTGCTGTGGGTGG-----TCGCGCGGCGCTTA-GCCAGT 144
QY 87 SerSerThrArgGlyAlaAlaGlyLeuAspGlyLysGlyAArgAspMetLaspGluAlaGly 106
Db 145 GACAGACAGCAGCGCGCCGACGAGATTAAAT----- 174
QY 107 AsnHieArgSerGlnGlnThrAsnThrGlyThrGluAsnGlnThrLeuHieValLeuThr 126
Db 175 -----GAT 177
QY 127 GlnTyArgLeuValSerAlaTyArgLysValAspHieArgGlyAAspTyValSerHieGln 146
Db 178 GATTAGCTCTTTTCTCAGCCAGTAGAAGTAGACTCAGCGGTCATATATTTCACACGAC 237
QY 147 IleMetHieHieGlnArgArgArgAlaValAlaValSerGluValGluSerLeuHie 166
Db 238 ATTTTSCACACGCGCGAAGAAAGCGATCG--GCCAGAAATCCAGAAAGCTCCCTGCGAC 294
QY 167 LeuArgLeuLysGlyProArgHieAspPheHieMetAspLeuArgThrSerSerLeu 186
Db 295 TACCGATTTCACACTTTGGACAGAACTGCACTTGAACTTAAG--CCCTCGCGGATT 351
QY 187 ValAlaProGlyPheIleValGlnThrLeuGlyLysThrGlyThrLysSerValGlnThr 206
Db 352 TTGACAGATCACTTATTGTCCAGTACTTGAAAGATGTGCTTCAAGACTCAGAA 411
QY 207 LeuProProGluAspPheCysPheTyArgGlnGlySerLeuArgSerHieArgAsnSerPro 226
Db 412 ---CCGAGGTGACAGAAATGCTTCTATCAGGGATTATACAGAAATGAC--AGCTCTCTCC 465
QY 227 SerHieGlyGlyLysPheCysGlnGlySerThrArgThrLeuLysLeuCysAsnSerGln 246
Db 466 TCTGTGGCTGTCTACGCTGTCTGCTGTCTCAGGTTTAATAGACACAGAAATGAA 525
QY 247 -----LysCysProArgAspSerValAspPheArgAlaAlaGlnCysAlaGln 262
Db 526 TTCCTCATCTCGGCATTACCTCAG-----CTTCTGGCCGACGAA 564
QY 263 HieAsnSerArgArgPheArgGlyArgArgHieTyTyLysTrpLysProTyThrGlnValGlu 282
Db 565 CACAACTACAGCTCCCTCGGGGTACACAT-----CTTCACGTAAT-GTACAA 611
QY 283 AlaAspLeuCysLysLeuTyTyLysIleAlaGlnGlyPheAsp----- 296
Db 612 AAGGAC-----ACGACAGGAGAAATCCACGCGTACCGTGGCTA 650
QY 297 -----PhePhePheSerLeuSerAsnLysVal--LysAspGlyThrProCysSerGln 313
Db 651 CCCCGGCTCTGGCGGGAATATATCTGATTACTCCCAAGTCATATCCCATCATCTCA 710
QY 314 AspSerArgAsn---ValCysIleAspGlyIleCysGluLeuSerValVal---SerThr 331
```

```
Db 711 GAGTCGAGAGACAGAGTATCACCAATCGAAGGTGGCAAAAGCAGATTTTGTGCGACGAG 770
QY 332 -SerAlaHieMetProGlnProTyArgLysLeuAspPheIleLeuProAspGlyTyTyLys 351
Db 771 CAAAGAAATATGTCTCCCAAGCTCCCAAGAGACACATATCTTAAGTTTGATGAATATAG 830
QY 351 sSerCysLeuArgHieLysValArgSerLeuLeuArgSerHieArgAsnGlnGluLeuAsnVa 371
Db 831 GAGCTCTGGCGACCCAGCAAGATCAGTGGAAATATCAGAAAGGCG-----CTCAATGT 884
QY 371 GlnThrLeuValValValAspLysLysMetGlnAsnHieSGlyHieGlnLysLeuH 391
Db 885 GGAACCCCTCGTGGTGGCAGACAGAAATATGTGAAAGACATGGCAGAGGAATGTCTAC 944
QY 391 rThrTyValLeuThrHieLeuAsnMetValSerAlaLeuPheLysAspGly----- 408
Db 945 CACATACATCTCAACAGTAATACATGTTTCTGCGCTATTTAAAGATGGACATATTGG 1004
QY 408 ----- 408
Db 1005 AAGTACATAAACGTGTGTGTGTGAGCCTAATCTCTGAAACAAGAACTGAGAGATT 1064
QY 409 -----Le 409
Db 1065 ATTTGATCAACCATATCGACAGACAGCTCTGTGAATGTTTTGTCAATGGCAGCTGCGCT 1124
QY 409 UMetGlyLysAspGlyThrArgHieAspHieValIleLeuLeuThrGlyLeuAspIleCys 429
Db 1125 CATTTGAAAGATGGCAGAGACAGCATGATCCATCTTACACAGATTTTGATATTGG 1184
QY 429 sSerTrpLysAsnGluProCysAspTrpLeuGlyPheAlaProIleSerGlyMetCysSe 449
Db 1185 TTCTTGGAAAGATGAACATGTGACACTTAGGGTTTCCCCCATCAGTGAATGTGCTC 1244
QY 449 rTyTyTyArgSerCysThrIleAsnGluAspThrGlyLysGlyLysAlaPheThrIleAl 469
Db 1245 TAAAGTCCAGAGTTTATCCATATGAAGACACAGACTTGGCTTGGCTTACCAATGCC 1304
QY 469 sHieGluSerGlyHieAsnPheGlyMetIleHieAspGlyGlnGlyLysAsnMetCysLysLys 489
Db 1305 TCATAGATCAGGCGACAACTTTGGTATGATTCAGCAGCGAAGAGGAATCCCTGCAGAAA 1364
QY 489 sSerGlnGlyAsnIleMetSerProThrLeuAlaGlyArgAsnGlyValPheSerTrpSe 509
Db 1365 GCGTGAAGGCATATACATGTCTCCACACTGACCGGAAACATGAGATGTTTTCATGTGC 1424
QY 509 rProCysSerArgGlnTyTyLeuHieLysPheLeuSerThrAlaGlnAlaIleCysLeuAl 529
Db 1425 TTCCTGACGCGCCAGTATCTCAGAAATCTCTCAGACACCTCAGCGGGGTGTCTAGT 1484
QY 529 sAspGlnProLysProValLysGlyTyTyTyTyTrpGlnLysLeuProGlyGlyLeuTy 549
Db 1485 GGAATAGGCCCAAGACAGACAGACAGTATTAATATCCGACAAACATACAGACAGATTTA 1544
QY 549 rAspAlaAsnThrGlnCysLysTrpGlnPheGlyGlyLysValLysLeuCysMetLeuAs 569
Db 1545 TGATCTGACACACAGTGTAAATGGCAATTGGACAAAGCCAAAGTATATGACGCTTGG 1604
QY 569 rPheLysLysAspIleCysLysValLeuTrpCysHieArgIleGlyArgLysCysGlnTh 589
Db 1605 TTTTGTGAAGATATTCAAATCACTTTGGTGGCCAGGAGTGAAGCCACAGGTGTGAGAC 1664
QY 589 rLysPheMetProAlaAlaGlnGlyThrIleCysGlyHieAspMetTrpCysArgGlyGly 609
Db 1665 CAAATTATAGCCCGGACAGACAGAAAGGACCGTTTGTGCTTGAGTATGTGTGTGCGCAAG 1724
QY 609 rGlnCysValLysTyTyLysAspGlnGlyProLysProThrHieGlyHieTrpSerAspTr 629
Db 1725 CCAATGCGCTAAAGTTTGGGAGCTCGGGCCCGCCATTCACGCGCCAGTGTCCGCGCTG 1784
QY 629 rSerSerTrpSerProCysSerArgTrpThrCysGlyGlyLysValSerHieArgSerArgLe 649
```

```
Db      1785 GTGAAAGTGTCAAGATGTTCCCGACATGTGTCGAGCACTAAGTTCAGAGAGACAA 1844
Qy      649 uCyThrAsnProLyseProSerHisGlyGlyLeuPheCysGluGlySerThrArgThrLe 669
      1845 CTCGATTAACCCCAAGCTCAGTATGCTGCTTATTTCTGCCAGTTCTAGCCGATTTA 1904
Qy      669 uLyLeuCyAsnSerGlnLyseProArgAspSerValAspPheArgAlaIaGlnCy 689
      1905 TCAGCTGTGCAATATTAACCTTCGCAATGAATAATAGCTTGATTTTGGGCTCAACAGTG 1964
Qy      689 ValAlaGlnHisAsnSerArgArgPheArgGlyArgHisIleTyrLeuIleTyrProTyrThrGln 709
      1965 TGGAGATATATAACGCAAACTTTCTCGTAGAGTTCTTACAGAGGAAACCTATACAA 2024
Qy      709 nValGluAspGlnAspLeuCyAsyLeuTyrCysIleAlaGlyGlyPheAspPhePheP 729
      2025 AGTGGAAAGAGAAATGATGATGCAAACTGTACTGCAAGGCTGAGAAACTTTGAAATTTT 2084
Qy      729 eSerLeuSerAsnLyseValLyseAspGlyThrProCysSerGlyAspSerArgAsnValCy 749
      2085 TGCATATGTCGGCAAGTGAAGATGGAATCTCCCTGCTCCCAACAAATAGATGTTTG 2144
Qy      749 sIleAspGlyIleCysGluArgValGlyCysAspAsnValLeuGlySerArgAlaValGln 769
      2145 TATTTACGGGGGTTTGTGAACCTAGTGGATGTGATCATGAACTAGGCTCTAAACAGTTTC 2204
Qy      769 uAspValCysGlyValCysAsnGlyAsnAsnSerAlaCysThrIleHisArgGlyLeuTyr 789
      2205 AGATGCTGTGGGGGTTTGCAAAGGTGATTAATTCACCTTGCAAGTTTATTAAGGCTGTA 2264
Qy      789 rThrLyAsnHisHisIleThrAsnGlnTyrTyrHisMetValThrIleProSerGlyAlaArg 809
      2265 CTCACACACAGATTAAGCAATGAATGATTAATCCGGTGTCAATTCACAGCTGGCCGCG 2324
Qy      809 gSerIleArgIleTyrGlyMetAsnValSerThrSerTyrIleSerValArgAsnAlaLe 829
      2325 AACCATCTGAATCGAGAGCTGAGGATTCCTTCAGATTCCTGCACTTGGAAGCTCAG 2384
Qy      829 uAGSArgTyrTyrLeuAsnGlyHisIleThrValAspTyrProGlyArgTyrLysePhe 849
      2385 TCAAAGTATTAACCTCCACGGGGGCTGAGACATGCACTGGCTGGGAGATTCCTTCCG 2444
Qy      849 rGlyThrThrPheAspTyrArgArgSerTyrAsnGluProGluAsnLeuIleAlaThrGln 869
      2445 TGGAGACACGTTTGAAATACAGAGCTCTTTCACACGGCCGGAACGTGTGAAGGCGAG 2504
Qy      869 yProThrAsnGlnThrLeuIleValGlyLeuLeuPheGlnGlyArgAsnProGlyValAl 889
      2505 GCCCACAATGAAGACGCTGCTTTGAAATCTGATGCCAAGGCAMAATCCAGGAGATAGC 2564
Qy      889 sTrpGluTyrSerMetProArgLeu-----GlyThrGluLyseGlnProProAla----- 965
      2565 TTGAAGTATGCACTTCCCAAGGTCATGAATGGAAC-----CCACAGCACACAA 2615
Qy      906 -GlnProSerTyrThrTrpAlaIleValArgSerGluCysSerValSerCysGlyGlyGln 925
      2616 AAGACCGCTATACCTGAGATACGTCGAGTACAGATGCTCGCTCCCTGCTGAGAG 2675
Qy      925 Y 925
Db      2676 T 2676
```

```

; PRIOR APPLICATION NUMBER: 60/353,680
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-354-983-3

Alignment Scores:
Pred. No.: 1,07e-242 Length: 3219
Score: 2440.00 Matches: 471
Percent Similarity: 65.89% Conservative: 124
Best Local Similarity: 52.16% Mismatches: 190
Query Match: 46.60% Indels: 119
DB: 18 Gaps: 18

US-09-981-151D-8 (1-952) x US-10-354-983-3 (1-3219)
Qy      85 AlaSerSerThrArgGlyAlaAlaGlyLeuAspGlyLyseGlyArgAspMetAspGlu 104
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      70 GCCAGTGAACGACGACGACGCGCCGACGAGTTAAAT----- 105
Qy      105 AlaGlyAsnHisArgSerGlnInThrAsnThrGlyThrGluAsnGlnThrLeuHisVal 124
      ----- 105
Db      105 ----- 105
Qy      125 LeuThrGlnTyrAspLeuValSerAlaTyrGluValAspHisArgGlyAspTyrValSer 144
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      106 ---GATGATTAACCTTTTGTACAGCCAGTAGAAGTGAAGTCAAGCCGGGTCAATATTTTCA 162
Qy      145 HisGluIleMetHisHisIleArgArgArgArgAlaValAlaValSerGluValGluSer 164
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      163 CAGCAATTTTGCACACGCGAGAAAGGATGCG---CGCGAATGCCAAGACTCC 219
Qy      165 LeuHisLeuArgLeuLyseGlyProArgHisAspPheHisMetAspLeuArgThrSerSer 184
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      220 CTCGATTAACGATTTTCAAGATTTGACAGAACTCAGCTTAAGAACTTAAG---CCCTCG 276
Qy      185 SerLeuValAlaProGlyPheIleValGlnThrLeuGlyLyseThrGlyThrLyseSerVal 204
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      277 GCGATTTTGAAGCATCACTTATTTGCCAGGTACTTGGAAGATGCTGCTTCAGAGACT 336
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      205 GlnThrLeuProProGluAspPheCysPheTyrGlnGlySerLeuArgSerHisArgAsn 224
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      337 CAGAAA---CCGAGGTGACGACATGCTTTATCAGGATTTATCGAATGAC---AGC 390
Qy      225 SerProSerHisGlyGlyLysePheCysGluGlySerThrArgThrLeuLyseCysAsn 244
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      391 TCCTCCTGTGCTGTGCTGTGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 450
Qy      245 SerGln-----LysCysProArgAspSerValAspPheArgAlaIaGlnCys 260
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      451 AATGAATTCCTCATCTCGCATTAACCTCAG-----CTTCTGAGCC 489
Qy      261 AlaGlnHisAsnSerArgArgPheArgGlyArgHisIleTyrLeuTyrProTyrThrGln 280
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      490 CAGAAACACACACACAGCTCCCTCGGGATCACAT-----CTTCAGTACT- 536
Qy      281 ValGluAlaAspLeuCyAsyLeuTyrCysIleAlaGluGlyPheAsp----- 296
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      537 GTACAAAGGAC-----ACGAGAGAGAAATCCAGGCGTACCG 575
Qy      297 -----PhePheSerLeuSerAsnLyseVal---LysAspGlyThrProCys 311
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      576 TGGCTACCCCGGCTCGCGCGAATATCTGGTTATCTCCCAAGTCAACATTCGCCATCG 635
Qy      312 SerGluAspSerArgAsn---ValCysIleAspGlyIleCysGluLeuSerValVal--- 329
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      636 ATCTCAAGTCGAGACACAGATGATCACAATGCAAGGTGCAAAACAGCATTTTGTGG 695
Qy      330 SerThr-SerAlaHisMetProGlnProLyseGluAspLeuPheIleLeuProAspGln 349
```

```
Db 696 ACACGCGAAGAAATATGCTCCCAAGCCTCCACAGAGGACACCTATCTAAGGTTTATGA 755
QY 349 uTyrLysSerCysLeuArgHisIlyAsrSerLeuLeuArgSerHisArgAangluGule 369
Db 756 ATATGGAGAGCTCTGGGCGACCCAGAAAGATACGCTGGAAAATCCAAAAGGCG-----CT 809
QY 369 uAenValGluThrLeuValValValAspLysLysMetGlnAsnHisGluIleAspLys 389
Db 810 CAATGTGAAAACCCCTGGTGGTGGCAGCAAGAAAATGTGTGAAAACATGCGCAAGGGAAA 869
QY 389 nileThrThrValLeuThrIleLeuAsnMetValSerAlaLeuPheLysAspGly-- 408
Db 870 TGTACCAACATACATCTCACAGTAATGAACATGTTCTGCGCTATTAAAGATGGAGC 929
QY 408 ----- 408
Db 930 TATTGGAAGTACATAAAGCTGGTGTGTGAGCCTAATTCTTGTGAACAAAGACCTGG 989
QY 408 ----- 408
Db 990 AGGATTATTGATCAACATCATGACAGACAGCTCTGTAATAGTTTGTCAATGGCAGTC 1049
QY 409 ----LeuMetGluLysAspGlyThrArgHisAspHisAlaIleLeuLeuThrGlyLeuAs 427
Db 1050 TGGCCTCATTTGGAAAGATGGCAAGAGACATGATCATGCCATCTTAACAGAGATTTGA 1109
QY 427 rIleCysSerTrpLysAsnGluProCysAspThrLeuGlyPheAlaProIleSerGlyMe 447
Db 1110 TATTGTCTTGTGGAAAGATGAACCATGTGACATCTAGGCTTTGCCCATCATGCTGAAT 1169
QY 447 tCysSerLysTrpArgSerCysThrIleAsnGluAspThrGlyLeuGlyLeuAlaPheTh 467
Db 1170 GTGCTCTAAGTACCGAAGTTGTACATATGAGACACAGGACTTGCGCTTGCTTCAC 1229
QY 467 rIleAlaHisGluSerGlyHisAsnPheGlyMetIleHisAspGluGluGlyAsnMetCys 487
Db 1230 CATGCTCATGATCGAGGACACACTTTGGTATGATTCACAGAGGAGAAAGGAGATCCCTG 1289
QY 487 sIlyLysSerGluGlyAsnIleMetSerProThrLeuAlaGlyArgAsnGlyValPheSe 507
Db 1290 CAGAAAGGCTGAAAGGCAATATCATGCTCTCCACATGACCGGAAACATGGAGTGTTC 1349
QY 507 rTrpSerProCysSerArgGlnTrpLeuHisLysPheLeuSerThrAlaGlnAlaIleCys 527
Db 1350 ATGGCTCTTCTTGACGCGCCAGATATCTCAAGAAATCTCTACAGCACCTCAGCGGGCTG 1409
QY 527 sIleuAlaAspGlnProLysProValLysGluTrpLysTrpProGluLysLeuProGly 547
Db 1410 TCTAGTGAATGAGCCCAAGGACAGACGAGATTAATATCCGGACAAACTACACAGGACA 1469
QY 547 uLeuTrpAspAlaAsnThrGlnCysLysTrpGlnPheGlyGluLysValLysLeuCysMe 567
Db 1470 GATTATGATGCTGACACACAGGTAAATGGCAATTTGGAGCAAAAGCCAAAGTTATGCG 1529
QY 567 tLeuAspPheLysLysAspLysCysLysValLysLeuTrpCysHisArgIleGlyArgLysCys 587
Db 1530 CCTTGGATTGTGAAGAGATATTGCAAAATCACTTGTGTCCACCGGATGGCGACAGGCTG 1589
QY 587 sGluThrLysPheMetProAlaAlaGluGlyThrIleCysGlnHisAspMetTrpCysArg 607
Db 1590 TGAAGACCAAGTTTATGCCCCGACAGAGAGGACCGTTGTGGCTTGAAGTATGGGTGCG 1649
QY 607 gGlyGlyGlnCysValLysValLysAspGluGlyProLysProThrHisGlyHisTrpSe 627
Db 1650 GCAAGGCGCAGTGGCTAAAGTTTGGGAGCGTCGGGCGCCCGCCATGCAAGGCAAGTGCCTC 1709
QY 627 rAspTrpSerSerTrpSerProCysSerArgThrCysGlyGlyGlyValSerHisArgSe 647
Db 1710 CCGCTGTGTGAAGTGTCAAGATGTTCCTCGGACATGTGTGTGAGGAGTCAAGTTCCAGGA 1769
QY 647 rArgLeuCysThrAspProLysProSerHisGlyGlyLysPheCysGluGlySerThrArg 667
```

```
Db 1770 GAGACATGCAATTAACCCCAAGCCTCAGTAGTGGCATATTCTGTCCAGGTTTACGCCG 1829
QY 667 gThrLeuLysLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaI 687
Db 1830 TATTATTCAGCTGTGCATATTTAACTTGAACCTTGCATATGAATAAGCTTGATTTTCCGGCCCA 1889
QY 687 aGlnCysAlaGluHisAsnSerArgArgPheArgGlyArgHisIlyLysTrpLysProTy 707
Db 1890 ACAGTGTGCAGAAATTAACAGCAAACTTTCCGTGAGTGTCTTACAGTGGAAAACCTTA 1949
QY 707 rThrGlnValGluAspGluAspLeuCysLysLeuLysLeuTrpCysHisAlaGluGlyPheAsp 727
Db 1950 TCAAAAGGTGAAGAGAAAGATCGATGCAAACTGATGCAAGGCTGCAAGACTTTGAAT 2009
QY 727 ePhePheSerLeuSerAsnLysValLysAspGlyThrProCysSerGluAspSerArgAs 747
Db 2010 TTTTGTTCGAATGTCCGGCAAAAGTGAAGATGGAATCCCTGCTCCCAACAGAAATGA 2069
QY 747 nValCysIleAspGlyIleCysGluArgValGlyCysAspAsnValLysGlySerAspAl 767
Db 2070 TGTGTGTATTTGACGGGGTGTGTGAATGATGGAGATGATCATGAACTAAGGCTTAAGC 2129
QY 767 aValGluAspValCysGlyValCysAsnGlyAsnAsnSerAlaCysThrIleHisArgG 787
Db 2130 AGTTCAAGTCTGTGTGGCGTTTGCAAAGGTGATATTCAACTTGCAAGTTTATTAAGG 2189
QY 787 yLeuTrpThrLysHisHisIleHisThrAsnGlnTrpTrpHisMetValThrIleProSerG 807
Db 2190 CCTGTATCTCAACAGCAATTAAGCAATGAAATATTAATCCGGTGTGCATCTTCCAGCTGG 2249
QY 807 yAlaArgSerIleArgGlyIleTrpGluMetAsnValSerThrSerTrpIleSerValArgAs 827
Db 2250 CCGCCGGAAGCATCGAAATCCAGAGACTCAGGTTTCCCTCCAGTTACCTCCGCAAGGTCGAAG 2309
QY 827 nAlaLeuArgArgTrpTrpLeuAsnGlyHisIleTrpThrValAspTrpProGlyArgTrpLys 847
Db 2310 CCTCAGTCAAAAGTATTACTTCAACCGGGGCTGAGACATCGACTGAGCTGGGGAATTCCC 2369
QY 847 sPheSerGlyThrThrPheAspTrpArgArgSerTrpAsnGluProGluAsnLysIleAl 867
Db 2370 CTTCCTGGAGACAGTTTGAATATCACAGCGCTCTTAACCGCCGGAACGCTGTACGCC 2429
QY 867 aThrGlyProThrAsnGluThrIleuIleValGluLeuLeuPheGlnGlyArgAsnProG 887
Db 2430 GCCAGGGCCCAAAATGAGAGCGTGTCTTGAATTTGTGATGCAAGGCAAAATCCAGG 2489
QY 887 yValAlaTrpGluTrpSerMetProArgLeu-----GlyThrGluLysGlnProProAl 905
Db 2490 GATACCTTGAAGATATGCACTTCCCAAGGTCAATGAATGAAGT-----CAACCAAGC 2540
QY 905 a-----GlnProSerTrpThrTrpAlaIleValArgSerGluCysSerValSerCysG 923
Db 2541 CACAAAAGACTCGCTTATACCTGGAATATCGTGAAGTCAAGAGTCTCCGTCTCCGTGG 2600
QY 923 yGlyGly 925
Db 2601 TGGAGGT 2607
```

Search completed: September 10, 2005, 03:04:41  
Job time : 1388 secs